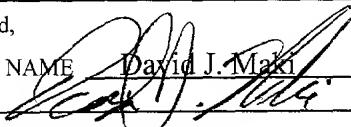


UTILITY PATENT APPLICATION TRANSMITTAL		Attorney Docket No. 210121.419C7
		First Inventor or Application Identifier Tony N. Frudakis
		Title COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
		Express Mail Label No. EL487465173US
APPLICATION ELEMENTS <small>See MPEP chapter 600 concerning utility patent application contents.</small>		ADDRESS TO: Box Patent Application Assistant Commissioner for Patents Washington, D.C. 20231
<p>1. <input type="checkbox"/> General Authorization Form & Fee Transmittal (Submit an original and a duplicate for fee processing)</p> <p>2. <input checked="" type="checkbox"/> Specification [Total Pages] 57 <ul style="list-style-type: none"> - Descriptive Title of the Invention - Cross References to Related Applications - Statement Regarding Fed sponsored R & D - Reference to Microfiche Appendix - Background of the Invention - Brief Summary of the Invention - Brief Description of the Drawings (if filed) - Detailed Description - Claim(s) - Abstract of the Disclosure </p> <p>3. <input checked="" type="checkbox"/> Drawing(s) (35 USC 113) [Total Sheets] 25</p> <p>4. Oath or Declaration [Total Pages] <input type="text"/></p> <p>a. <input type="checkbox"/> Newly executed (original or copy)</p> <p>b. <input type="checkbox"/> Copy from a prior application (37 CFR 1.63(d)) (for continuation/divisional with Box 17 completed) <ul style="list-style-type: none"> i. <input type="checkbox"/> DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b) </p> <p>5. <input type="checkbox"/> Incorporation By Reference (useable if box 4b is checked) The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered to be part of the disclosure of the accompanying application and is hereby incorporated by reference therein.</p> <p>6. <input type="checkbox"/> Microfiche Computer Program (Appendix)</p> <p>7. Nucleotide and Amino Acid Sequence Submission (if applicable, all necessary) <ul style="list-style-type: none"> a. <input checked="" type="checkbox"/> Computer-Readable Copy b. <input checked="" type="checkbox"/> Paper Copy (identical to computer copy) c. <input checked="" type="checkbox"/> Statement verifying identity of above copies </p>		
ACCOMPANYING APPLICATION PARTS		
<p>8. <input type="checkbox"/> Assignment Papers (cover sheet & document(s))</p> <p>9. <input type="checkbox"/> 37 CFR 3.73(b) Statement (when there is an assignee) <input type="checkbox"/> Power of Attorney</p> <p>10. <input type="checkbox"/> English Translation Document (if applicable)</p> <p>11. <input type="checkbox"/> Information Disclosure Statement (IDS)/PTO-1449 <input type="checkbox"/> Copies of IDS Citations</p> <p>12. <input type="checkbox"/> Preliminary Amendment</p> <p>13. <input checked="" type="checkbox"/> Return Receipt Postcard</p> <p>14. <input type="checkbox"/> Small Entity Statement(s) <input type="checkbox"/> Statement filed in prior application, Status still proper and desired</p> <p>15. <input type="checkbox"/> Certified Copy of Priority Document(s) (if foreign priority is claimed)</p> <p>16. <input checked="" type="checkbox"/> Other: <u>Certificate of Express Mail</u></p>		
<p>17. If a CONTINUING APPLICATION, check appropriate box and supply the requisite information below and in a preliminary amendment</p> <p><input type="checkbox"/> Continuation <input type="checkbox"/> Divisional <input checked="" type="checkbox"/> Continuation-In-Part (CIP) of prior Application No. 09/429,755</p> <p>Prior application information: Examiner <u>(NOT ASSIGNED)</u> Group / Art Unit <u>1641</u></p> <p><input type="checkbox"/> Claims the benefit of Provisional Application No. _____</p>		
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Respectfully submitted,

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REGISTRATION NO. 31,392Date MARCH 25, 2000

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

PATENT

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Respectfully submitted,

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Judith A. Breaks/Jeanette West/Susan Johnson

Enclosures:

Postcard
Form PTO/SB/05
Specification, Claims, Abstract (57 pages)
25 pages of Drawings (Figs. 1-24)
Declaration re Sequence Listing
Computer Diskette Containing Sequence Listing
Hard Copy of Sequence Listing (112 pages)

COMPOSITIONS AND METHODS FOR THE TREATMENT
AND DIAGNOSIS OF BREAST CANCER

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of U.S. Patent Application No. 5 09/429,755, filed October 28, 1999, which is a continuation-in-part of U.S. Patent Application No. 09/289,198, filed April 9, 1999, which is a continuation-in-part of U.S. Patent Application No. 09/062,451, filed April 17, 1998, which is a continuation in part of U.S. Patent Application No. 08/991,789, filed December 11, 1997, which is a continuation-in-part of U.S. Patent Application No. 08/838,762, filed April 9, 1997, 10 which claims priority from International Patent Application No. PCT/US97/00485, filed January 10, 1997, and is a continuation-in-part of U.S. Patent Application No. 08/700,014, filed August 20, 1996, which is a continuation-in-part of U.S. Patent Application No. 08/585,392, filed January 1, 1996.

TECHNICAL FIELD

15 The present invention relates generally to the detection and therapy of breast cancer. The invention is more specifically related to nucleotide sequences that are preferentially expressed in breast tumor tissue and to polypeptides encoded by such nucleotide sequences. The nucleotide sequences and polypeptides may be used in vaccines and pharmaceutical compositions for the prevention and treatment of breast 20 cancer. The polypeptides may also be used for the production of compounds, such as antibodies, useful for diagnosing and monitoring the progression of breast cancer in a patient.

BACKGROUND OF THE INVENTION

Breast cancer is a significant health problem for women in the United 25 States and throughout the world. Although advances have been made in detection and treatment of the disease, breast cancer remains the second leading cause of cancer-related deaths in women, affecting more than 180,000 women in the United States each year.

For women in North America, the life-time odds of getting breast cancer are now one in eight.

No vaccine or other universally successful method for the prevention or treatment of breast cancer is currently available. Management of the disease currently 5 relies on a combination of early diagnosis (through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. *See, e.g.*, Porter-Jordan and 10 Lippman, *Breast Cancer* 8:73-100 (1994). However, the use of established markers often leads to a result that is difficult to interpret, and the high mortality observed in breast cancer patients indicates that improvements are needed in the treatment, diagnosis and prevention of the disease.

Accordingly, there is a need in the art for improved methods for therapy 15 and diagnosis of breast cancer. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the subject invention provides compositions and methods for the diagnosis and therapy of breast cancer. In one aspect, isolated polynucleotides are 20 provided, comprising (a) a nucleotide sequence preferentially expressed in breast cancer tissue, relative to normal tissue; (b) a variant of such a sequence, as defined below; or (c) a nucleotide sequence encoding an epitope of a polypeptide encoded by at least one of the above sequences. In one embodiment, the isolated polynucleotide comprises a human endogenous retroviral sequence recited in SEQ ID NO:1. In other embodiments, 25 the isolated polynucleotide comprises a sequence recited in any one of SEQ ID NO: 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

In related embodiments, the isolated polynucleotide encodes an epitope of a polypeptide, wherein the polypeptide is encoded by a nucleotide sequence that: (a) hybridizes to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 under stringent conditions; and (b) is at least 80% identical to a sequence recited in any one of SEQ ID NO: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

In another embodiment, the present invention provides an isolated polynucleotide encoding an epitope of a polypeptide, the polypeptide being encoded by: (a) a nucleotide sequence transcribed from the sequence of SEQ ID NO: 141; or (b) a variant of said nucleotide sequence that contains one or more nucleotide substitutions, deletions, insertions and/or modifications at no more than 20% of the nucleotide positions, such that the antigenic and/or immunogenic properties of the polypeptide encoded by the nucleotide sequence are retained. Isolated DNA and RNA molecules comprising a nucleotide sequence complementary to a polynucleotide as described above are also provided.

In related aspects, the present invention provides recombinant expression vectors comprising a polynucleotide as described above and host cells transformed or transfected with such expression vectors.

In further aspects, polypeptides comprising an amino acid sequence encoded by a polynucleotide as described above, and monoclonal antibodies that bind to such polypeptides are provided. In certain embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 299, 300, 304-306, 308 and 315, and variants thereof as defined below.

In yet another aspect, methods are provided for determining the presence of breast cancer in a patient. In one embodiment, the method comprises detecting, within a biological sample, a polypeptide as described above. In another embodiment, the

method comprises detecting, within a biological sample, an RNA molecule encoding a polypeptide as described above. In yet another embodiment, the method comprises (a) intradermally injecting a patient with a polypeptide as described above; and (b) detecting an immune response on the patient's skin and therefrom detecting the presence of breast cancer in the patient. In further embodiments, the present invention provides methods for determining the presence of breast cancer in a patient as described above wherein the polypeptide is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In a related aspect, diagnostic kits useful in the determination of breast cancer are provided. The diagnostic kits generally comprise either one or more monoclonal antibodies as described above, or one or more monoclonal antibodies that bind to a polypeptide encoded by a nucleotide sequence selected from the group consisting of sequences provided in SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and a detection reagent.

Diagnostic kits are also provided that comprise a first polymerase chain reaction primer and a second polymerase chain reaction primer, at least one of the primers being specific for a polynucleotide described herein. In one embodiment, at least one of the primers comprises at least about 10 contiguous nucleotides of a polynucleotide as described above, or a polynucleotide encoding a polypeptide encoded by a sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

Within another related aspect, the diagnostic kit comprises at least one oligonucleotide probe, the probe being specific for a polynucleotide described herein. In one embodiment, the probe comprises at least about 15 contiguous nucleotides of a polynucleotide as described above, or a polynucleotide selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217,

220, 241, 242 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289 and 290.

In another related aspect, the present invention provides methods for monitoring the progression of breast cancer in a patient. In one embodiment, the method 5 comprises: (a) detecting an amount, in a biological sample, of a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of polypeptide detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient. In another embodiment, the method comprises (a) detecting an amount, within a biological sample, of an RNA 10 molecule encoding a polypeptide as described above at a first point in time; (b) repeating step (a) at a subsequent point in time; and (c) comparing the amounts of RNA molecules detected in steps (a) and (b), and therefrom monitoring the progression of breast cancer in the patient. In yet other embodiments, the present invention provides methods for monitoring the progression of breast cancer in a patient as described above wherein the 15 polypeptide is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242, 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In still other aspects, pharmaceutical compositions, which comprise a 20 polypeptide as described above in combination with a physiologically acceptable carrier, and vaccines, which comprise a polypeptide as described above in combination with an immunostimulant or adjuvant, are provided. In yet other aspects, the present invention provides pharmaceutical compositions and vaccines comprising a polypeptide encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 78-86, 144, 145, 153, 167, 177, 193, 199, 205, 208, 215, 217, 220, 241, 242 and 246, 248, 249, 252, 256, 267, 270, 274, 277, 279, 282, 283, 285-287, 289, 290 and sequences that hybridize thereto under stringent conditions.

In related aspects, the present invention provides methods for inhibiting the development of breast cancer in a patient, comprising administering to a patient a 30 pharmaceutical composition or vaccine as described above.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

5 BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the differential display PCR products, separated by gel electrophoresis, obtained from cDNA prepared from normal breast tissue (lanes 1 and 2) and from cDNA prepared from breast tumor tissue from the same patient (lanes 3 and 4). The arrow indicates the band corresponding to B18Ag1.

10 Figure 2 is a northern blot comparing the level of B18Ag1 mRNA in breast tumor tissue (lane 1) with the level in normal breast tissue.

Figure 3 shows the level of B18Ag1 mRNA in breast tumor tissue compared to that in various normal and non-breast tumor tissues as determined by RNase protection assays.

15 Figure 4 is a genomic clone map showing the location of additional retroviral sequences obtained from ends of XbaI restriction digests (provided in SEQ ID NO:3 - SEQ ID NO:10) relative to B18Ag1.

Figures 5A and 5B show the sequencing strategy, genomic organization and predicted open reading frame for the retroviral element containing B18Ag1.

20 Figure 6 shows the nucleotide sequence of the representative breast tumor-specific cDNA B18Ag1.

Figure 7 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag1.

25 Figure 8 shows the nucleotide sequence of the representative breast tumor-specific cDNA B17Ag2.

Figure 9 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag2a.

Figure 10 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1b.

Figure 11 shows the nucleotide sequence of the representative breast tumor-specific cDNA B13Ag1a.

Figure 12 shows the nucleotide sequence of the representative breast tumor-specific cDNA B11Ag1.

5 Figure 13 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3c.

Figure 14 shows the nucleotide sequence of the representative breast tumor-specific cDNA B9CG1.

10 Figure 15 shows the nucleotide sequence of the representative breast tumor-specific cDNA B9CG3.

Figure 16 shows the nucleotide sequence of the representative breast tumor-specific cDNA B2CA2.

15 Figure 17 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA1.

Figure 18 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA2.

Figure 19 shows the nucleotide sequence of the representative breast tumor-specific cDNA B3CA3.

20 Figure 20 shows the nucleotide sequence of the representative breast tumor-specific cDNA B4CA1.

Figure 21A depicts RT-PCR analysis of breast tumor genes in breast tumor tissues (lanes 1-8) and normal breast tissues (lanes 9-13) and H₂O (lane 14).

25 Figure 21B depicts RT-PCR analysis of breast tumor genes in prostate tumors (lane 1, 2), colon tumors (lane 3), lung tumor (lane 4), normal prostate (lane 5), normal colon (lane 6), normal kidney (lane 7), normal liver (lane 8), normal lung (lane 9), normal ovary (lanes 10, 18), normal pancreases (lanes 11, 12), normal skeletal muscle (lane 13), normal skin (lane 14), normal stomach (lane 15), normal testes (lane 16), normal small intestine (lane 17), HBL-100 (lane 19), MCF-12A (lane 20), breast tumors (lanes 21-23), H₂O (lane 24), and colon tumor (lane 25).

30 Figure 22 shows the recognition of a B11Ag1 peptide (referred to as B11-8) by an anti-B11-8 CTL line.

Figure 23 shows the recognition of a cell line transduced with the antigen B11Ag1 by the B11-8 specific clone A1.

Figure 24 shows recognition of a lung adenocarcinoma line (LT-140-22) and a breast adenocarcinoma line (CAMA-1) by the B11-8 specific clone A1.

5 DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis, monitoring and therapy of breast cancer. The compositions described herein include polypeptides, polynucleotides and antibodies. Polypeptides of the present invention generally comprise at least a portion of a protein that is expressed at a greater level in human breast tumor tissue than in normal breast tissue (*i.e.*, the level of RNA encoding the polypeptide is at least 2-fold higher in tumor tissue). Such polypeptides are referred to herein as breast tumor-specific polypeptides, and cDNA molecules encoding such polypeptides are referred to as breast tumor-specific cDNAs. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of a polypeptide as described above, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or fragments thereof, that are capable of binding to a portion of a polypeptide as described above. Antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies.

Polypeptides within the scope of this invention include, but are not limited to, polypeptides (and epitopes thereof) encoded by a human endogenous retroviral sequence, such as the sequence designated B18Ag1 (Figure 5 and SEQ ID NO:1). Also within the scope of the present invention are polypeptides encoded by other sequences within the retroviral genome containing B18Ag1 (SEQ ID NO: 141). Such sequences include, but are not limited to, the sequences recited in SEQ ID NO:3 - SEQ ID NO:10. B18Ag1 has homology to the *gag* p30 gene of the endogenous human retroviral element S71, as described in Werner et al., *Virology* 174:225-238 (1990) and also shows homology to about thirty other retroviral *gag* genes. As discussed in more detail below, the present invention also includes a number of additional breast tumor-

specific polypeptides, such as those encoded by the nucleotide sequences recited in SEQ ID NO: 11-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 5 316 and 317.

As used herein, the term “polypeptide” encompasses amino acid chains of any length, including full length proteins containing the sequences recited herein. A polypeptide comprising an epitope of a protein containing a sequence as described herein may consist entirely of the epitope, or may contain additional sequences. The additional 10 sequences may be derived from the native protein or may be heterologous, and such sequences may (but need not) possess immunogenic or antigenic properties.

An “epitope,” as used herein is a portion of a polypeptide that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Epitopes may generally be identified using well known techniques, such as those 15 summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides derived from the native polypeptide for the ability to react with antigen-specific antisera and/or T-cell lines or clones. An epitope of a polypeptide is a portion that reacts with such antisera and/or T-cells at a level that is similar to the reactivity of the full length 20 polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold 25 Spring Harbor Laboratory, 1988. B-cell and T-cell epitopes may also be predicted via computer analysis. Polypeptides comprising an epitope of a polypeptide that is preferentially expressed in a tumor tissue (with or without additional amino acid sequence) are within the scope of the present invention.

The term “polynucleotide(s),” as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and 30 anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and corresponds to a DNA molecule in a generally one-to-one manner. An

mRNA molecule corresponds to an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes 5 all such operable anti-sense fragments.

The compositions and methods of the present invention also encompass variants of the above polypeptides and polynucleotides.

A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that 10 the antigenic properties of the polypeptide are retained. In a preferred embodiment, variant polypeptides differ from an identified sequence by substitution, deletion or addition of five amino acids or fewer. Such variants may generally be identified by modifying one of the above polypeptide sequences, and evaluating the antigenic properties of the modified polypeptide using, for example, the representative procedures 15 described herein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described below) to the identified polypeptides.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled 20 in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

25 Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. 30 The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance

binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity (determined as described below) to the recited sequence.

The breast tumor antigens provided by the present invention include variants that are encoded by DNA sequences which are substantially homologous to one or more of the DNA sequences specifically recited herein. "Substantial homology," as used herein, refers to DNA sequences that are capable of hybridizing under moderately stringent conditions. Suitable moderately stringent conditions include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5X SSC, overnight or, in the event of cross-species homology, at 45°C with 0.5X SSC; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. Such hybridizing DNA sequences are also within the scope of this invention, as are nucleotide sequences that, due to code degeneracy, encode an immunogenic polypeptide that is encoded by a hybridizing DNA sequence.

Two nucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acid residues in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of 5 evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) 10 Fast and sensitive multiple sequence alignments on a microcomputer *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) Optimal alignments in linear space *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) The neighbor joining method. A new method for reconstructing phylogenetic trees *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the 15 Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) Rapid similarity searches of nucleic acid and protein data banks *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison 20 of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which 25 the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity. In general, polynucleotides encoding all or a portion of the polypeptides described herein may be prepared using any 30 of several techniques. For example, cDNA molecules encoding such polypeptides may be cloned on the basis of the breast tumor-specific expression of the corresponding mRNAs, using differential display PCR. This technique compares the amplified

products from RNA template prepared from normal and breast tumor tissue. cDNA may be prepared by reverse transcription of RNA using a (dT)₁₂AG primer. Following amplification of the cDNA using a random primer, a band corresponding to an amplified product specific to the tumor RNA may be cut out from a silver stained gel and 5 subcloned into a suitable vector (e.g., the T-vector, Novagen, Madison, WI). Polynucleotides encoding all or a portion of the breast tumor-specific polypeptides disclosed herein may be amplified from cDNA prepared as described above using the random primers shown in SEQ ID NO.:87-125.

Alternatively, a polynucleotide encoding a polypeptide as described 10 herein (or a portion thereof) may be amplified from human genomic DNA, or from breast tumor cDNA, via polymerase chain reaction. For this approach, B18Ag1 sequence-specific primers may be designed based on the sequence provided in SEQ ID NO:1, and may be purchased or synthesized. One suitable primer pair for amplification from breast tumor cDNA is (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO:126) and 15 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO:127). An amplified portion of B18Ag1 may then be used to isolate the full length gene from a human genomic DNA library or from a breast tumor cDNA library, using well known techniques, such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (1989). Other sequences within the 20 retroviral genome of which B18Ag1 is a part may be similarly prepared by screening human genomic libraries using B18Ag1-specific sequences as probes. Nucleotides translated into protein from the retroviral genome shown in SEQ ID NO: 141 may then be determined by cloning the corresponding cDNAs, predicting the open reading frames and cloning the appropriate cDNAs into a vector containing a viral promoter, such as T7. 25 The resulting constructs can be employed in a translation reaction, using techniques known to those of skill in the art, to identify nucleotide sequences which result in expressed protein. Similarly, primers specific for the remaining breast tumor-specific polypeptides described herein may be designed based on the nucleotide sequences provided in SEQ ID NO:11-86, 142-298, 301-303, 307, 313, 314, 316 and 317.

30 Recombinant polypeptides encoded by the DNA sequences described above may be readily prepared from the DNA sequences. For example, supernatants

from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps 5 can be employed to further purify a recombinant polypeptide.

In general, any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide that 10 encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO.

Such techniques may also be used to prepare polypeptides comprising epitopes or variants of the native polypeptides. For example, variants of a native 15 polypeptide may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis, and sections of the DNA sequence may be removed to permit preparation of truncated polypeptides. Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to 20 those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc.* 85:2149-2146 (1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as 25 Perkin Elmer/Applied BioSystems Division, Foster City, CA, and may be operated according to the manufacturer's instructions.

In specific embodiments, polypeptides of the present invention encompass amino acid sequences encoded by a polynucleotide having a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 30 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307,

313, 314, 316 and 317, and variants of such polypeptides. Polypeptides within the scope of the present invention also include polypeptides (and epitopes thereof) encoded by DNA sequences that hybridize to a sequence recited in any one of SEQ ID NO:1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-
5 214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-
273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317
under stringent conditions, wherein the DNA sequences are at least 80% identical in overall sequence to a recited sequence and wherein RNA corresponding to the nucleotide sequence is expressed at a greater level in human breast tumor tissue than in normal
10 breast tissue. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2 X SSC, 0.1% SDS at 65°C. Polynucleotides according to the present invention include molecules that encode any of the above polypeptides.

15 In another aspect of the present invention, antibodies are provided. Such antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined
20 schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest
30 may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519 (1976), and improvements thereto. Briefly, these methods involve

the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a 5 myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, 10 aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing 15 hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and 20 extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Antibodies may be used, for example, in methods for detecting breast cancer in a patient. Such methods involve using an antibody to detect the presence or absence of a breast tumor-specific polypeptide as described herein in a suitable biological 25 sample. As used herein, suitable biological samples include tumor or normal tissue biopsy, mastectomy, blood, lymph node, serum or urine samples, or other tissue, homogenate, or extract thereof obtained from a patient.

There are a variety of assay formats known to those of ordinary skill in the art for using an antibody to detect polypeptide markers in a sample. *See, e.g.*, Harlow 30 and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, the assay may be performed in a Western blot format, wherein a protein

preparation from the biological sample is submitted to gel electrophoresis, transferred to a suitable membrane and allowed to react with the antibody. The presence of the antibody on the membrane may then be detected using a suitable detection reagent, as described below.

5 In another embodiment, the assay involves the use of antibody immobilized on a solid support to bind to the polypeptide and remove it from the remainder of the sample. The bound polypeptide may then be detected using a second antibody or reagent that contains a reporter group. Alternatively, a competitive assay 10 may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized antibody after incubation of the antibody with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the antibody is indicative of the reactivity of the sample with the immobilized antibody, and as a result, indicative of the concentration of polypeptide in the sample.

The solid support may be any material known to those of ordinary skill in 15 the art to which the antibody may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose filter or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. 20 Patent No. 5,359,681.

The antibody may be immobilized on the solid support using a variety of techniques known to those in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment 25 (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the antibody, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically 30 between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of antibody ranging

from about 10 ng to about 1 μ g, and preferably about 100-200 ng, is sufficient to immobilize an adequate amount of polypeptide.

Covalent attachment of antibody to a solid support may also generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the antibody. For example, the antibody may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (see, e.g., Pierce Immunotechnology Catalog and Handbook (1991) at A12-A13).

In certain embodiments, the assay for detection of polypeptide in a sample is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the biological sample, such that the polypeptide within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with breast cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by

assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of breast cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value established from non-tumor tissue. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without breast cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value may be considered positive for breast cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, p. 106-7 (Little Brown and Co., 1985). Briefly, in

this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for breast cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, the polypeptide within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of breast cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 1 μ g. Such tests can typically be performed with a very small amount of biological sample.

The presence or absence of breast cancer in a patient may also be determined by evaluating the level of mRNA encoding a breast tumor-specific polypeptide as described herein within the biological sample (e.g., a biopsy, mastectomy and/or blood sample from a patient) relative to a predetermined cut-off value. Such an 5 evaluation may be achieved using any of a variety of methods known to those of ordinary skill in the art such as, for example, *in situ* hybridization and amplification by polymerase chain reaction.

For example, polymerase chain reaction may be used to amplify sequences from cDNA prepared from RNA that is isolated from one of the above 10 biological samples. Sequence-specific primers for use in such amplification may be designed based on the sequences provided in any one of SEQ ID NO: 1, 11-86, 142-298 301-303, 307, 313, 314, 316 and 317, and may be purchased or synthesized. In the case of B18Ag1, as noted herein, one suitable primer pair is B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO:126) and B18Ag1-3 (5'CCG GTA TCT CCT 15 CGT GGG TAT T) (SEQ ID NO:127). The PCR reaction products may then be separated by gel electrophoresis and visualized according to methods well known to those of ordinary skill in the art. Amplification is typically performed on samples obtained from matched pairs of tissue (tumor and non-tumor tissue from the same 20 individual) or from unmatched pairs of tissue (tumor and non-tumor tissue from different individuals). The amplification reaction is preferably performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the tumor sample as compared to the same dilution of the non-tumor sample is considered positive.

As used herein, the term "primer/probe specific for a polynucleotide" 25 means an oligonucleotide sequence that has at least about 80% identity, preferably at least about 90% and more preferably at least about 95%, identity to the polynucleotide in question, or an oligonucleotide sequence that is anti-sense to a sequence that has at least about 80% identity, preferably at least about 90% and more preferably at least about 95%, identity to the polynucleotide in question. Primers and/or probes which may be 30 usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the polymerase chain reaction primers

comprise at least about 10 contiguous nucleotides of a polynucleotide that encodes one of the polypeptides disclosed herein or that is anti-sense to a sequence that encodes one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a 5 polynucleotide that encodes one of the polypeptides disclosed herein or that is anti-sense to a sequence that encodes one of the polypeptides disclosed herein. Techniques for both PCR based assays and *in situ* hybridization assays are well known in the art.

Conventional RT-PCR protocols using agarose and ethidium bromide staining, while important in defining gene specificity, do not lend themselves to 10 diagnostic kit development because of the time and effort required in making them quantitative (i.e., construction of saturation and/or titration curves), and their sample throughput. This problem is overcome by the development of procedures such as real time RT-PCR which allows for assays to be performed in single tubes, and in turn can be modified for use in 96 well plate formats. Instrumentation to perform such 15 methodologies are available from Perkin Elmer/Applied Biosystems Division. Alternatively, other high throughput assays using labeled probes (e.g., digoxigenin) in combination with labeled (e.g., enzyme fluorescent, radioactive) antibodies to such probes can also be used in the development of 96 well plate assays.

In yet another method for determining the presence or absence of breast 20 cancer in a patient, one or more of the breast tumor-specific polypeptides described may be used in a skin test. As used herein, a "skin test" is any assay performed directly on a patient in which a delayed-type hypersensitivity (DTH) reaction (such as swelling, reddening or dermatitis) is measured following intradermal injection of one or more polypeptides as described above. Such injection may be achieved using any suitable 25 device sufficient to contact the polypeptide or polypeptides with dermal cells of the patient, such as a tuberculin syringe or 1 mL syringe. Preferably, the reaction is measured at least 48 hours after injection, more preferably 48-72 hours.

The DTH reaction is a cell-mediated immune response, which is greater in 30 patients that have been exposed previously to a test antigen (i.e., an immunogenic portion of a polypeptide employed, or a variant thereof). The response may be measured visually, using a ruler. In general, a response that is greater than about 0.5 cm in diameter,

preferably greater than about 5.0 cm in diameter, is a positive response, indicative of breast cancer.

The breast tumor-specific polypeptides described herein are preferably formulated, for use in a skin test, as pharmaceutical compositions containing at least one polypeptide and a physiologically acceptable carrier, such as water, saline, alcohol, or a buffer. Such compositions typically contain one or more of the above polypeptides in an amount ranging from about 1 μ g to 100 μ g, preferably from about 10 μ g to 50 μ g in a volume of 0.1 mL. Preferably, the carrier employed in such pharmaceutical compositions is a saline solution with appropriate preservatives, such as phenol and/or 10 Tween 80TM.

In other aspects of the present invention, the progression and/or response to treatment of a breast cancer may be monitored by performing any of the above assays over a period of time, and evaluating the change in the level of the response (*i.e.*, the amount of polypeptide or mRNA detected or, in the case of a skin test, the extent of the 15 immune response detected). For example, the assays may be performed every month to every other month for a period of 1 to 2 years. In general, breast cancer is progressing in those patients in whom the level of the response increases over time. In contrast, breast cancer is not progressing when the signal detected either remains constant or decreases with time.

20 In further aspects of the present invention, the compounds described herein may be used for the immunotherapy of breast cancer. In these aspects, the compounds (which may be polypeptides, antibodies or polynucleotides) are preferably incorporated into pharmaceutical compositions or vaccines. Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable 25 carrier. Vaccines may comprise one or more such compounds in combination with an immunostimulant, such as an adjuvant or a liposome (into which the compound is incorporated). An immunostimulant may be any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. Examples 30 of immunostimulants include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example,

M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

Alternatively, a vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749 (1993), and reviewed by Cohen, *Science* 259:1691-1692 (1993). The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable

microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quill A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Corixa Corporation (Seattle, WA; *see* US Patent Nos.

4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555 and WO 99/33488. Immunostimulatory DNA sequences are also described, for example, 5 by Sato et al., *Science* 273:352, 1996. Another preferred adjuvant is a saponin, preferably QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less 10 reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Other preferred adjuvants include Montanide ISA 720 (Seppic, France), 15 SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Ribi ImmunoChem Research Inc., Hamilton, MT), RC-529 (Ribi ImmunoChem Research Inc., Hamilton, MT) and Aminoalkyl glucosaminide 4-phosphates (AGPs).

Any vaccine provided herein may be prepared using well known methods 20 that result in a combination of antigen, immunostimulant and a suitable carrier or excipient. The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following 25 administration). Such formulations may generally be prepared using well known technology (see, e.g., Coombes et al., *Vaccine* 14:1429-1438, 1996) and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by 30 a rate controlling membrane.

Carriers for use within such formulations are biocompatible, and may also

be biodegradable; preferably the formulation provides a relatively constant level of active component release. Such carriers include microparticles of poly(lactide-co-glycolide), as well as polyacrylate, latex, starch, cellulose and dextran. Other delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (e.g., a 5 cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (see e.g., U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of 10 the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells 15 that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (i.e., matched HLA 20 haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be 25 effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (see Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell 30 responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*,

and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

5 Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from 10 peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

15 Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high 20 expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

25 APCs may generally be transfected with a polynucleotide encoding a polypeptide of the present invention (or portion or other variant thereof) such that the polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. 30 Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo*

and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or 5 progenitor cells with the polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated 10 immunological partner, separately or in the presence of the polypeptide.

Vaccines and pharmaceutical compositions may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are preferably hermetically sealed to preserve sterility of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or 15 aqueous vehicles. Alternatively, a vaccine or pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

The above pharmaceutical compositions and vaccines may be used, for example, for the therapy of breast cancer in a patient. As used herein, a "patient" refers 20 to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with breast cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of breast cancer or to treat a patient afflicted with breast cancer. In a preferred embodiment, the compounds are administered either prior to or following surgical removal of primary tumors and/or treatment by 25 administration of radiotherapy and conventional chemotherapeutic drugs. To prevent or slow the development of breast cancer, a pharmaceutical composition or vaccine comprising one or more polypeptides as described herein may be administered to a patient. Alternatively, naked DNA or plasmid or viral vector encoding the polypeptide may be administered. For treating a patient with breast cancer, the pharmaceutical 30 composition or vaccine may comprise one or more polypeptides, antibodies or

polynucleotides complementary to DNA encoding a polypeptide as described herein (e.g., antisense RNA or antisense deoxyribonucleotide oligonucleotides).

Routes and frequency of administration, as well as dosage, will vary from individual to individual. In general, the pharmaceutical compositions and vaccines may 5 be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 10 doses may be administered for a 52-week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a 10 compound that, when administered as described above, is capable of promoting an anti-tumor immune response. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (e.g., more 15 frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 µg to 5 mg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 20 mL.

Polypeptides disclosed herein may also be employed in adoptive immunotherapy for the treatment of cancer. Adoptive immunotherapy may be broadly classified into either active or passive immunotherapy. In active immunotherapy, treatment relies on the *in vivo* stimulation of the endogenous host immune system to 25 react against tumors with the administration of immune response-modifying agents (for example, tumor vaccines, bacterial adjuvants, and/or cytokines).

In passive immunotherapy, treatment involves the delivery of biologic reagents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend 30 on an intact host immune system. Examples of effector cells include T lymphocytes (for example, CD8+ cytotoxic T-lymphocyte, CD4+ T-helper, tumor-infiltrating lymphocytes), killer cells (Natural Killer cells, lymphokine-activated killer cells), B

cells, or antigen presenting cells (such as dendritic cells and macrophages) expressing the disclosed antigens. The polypeptides disclosed herein may also be used to generate antibodies or anti-idiotypic antibodies (as in U.S. Patent No. 4,918,164), for passive immunotherapy.

5 The predominant method of procuring adequate numbers of T-cells for adoptive immunotherapy is to grow immune T-cells *in vitro*. Culture conditions for expanding single antigen-specific T-cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. These *in vitro* culture conditions typically utilize intermittent stimulation with antigen, often in the presence of cytokines, 10 such as IL-2, and non-dividing feeder cells. As noted above, the immunoreactive polypeptides described herein may be used to rapidly expand antigen-specific T cell cultures in order to generate sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage or B-cells, may be pulsed with immunoreactive polypeptides or transfected with a polynucleotide sequence(s), using 15 standard techniques well known in the art. For cultured T-cells to be effective in therapy, the cultured T-cells must be able to grow and distribute widely and to survive long term *in vivo*. Studies have demonstrated that cultured T-cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever et al. *Ibid*).

20 The polypeptides disclosed herein may also be employed to generate and/or isolate tumor-reactive T-cells, which can then be administered to the patient. In one technique, antigen-specific T-cell lines may be generated by *in vivo* immunization with short peptides corresponding to immunogenic portions of the disclosed polypeptides. The resulting antigen specific CD8+ CTL clones may be isolated from the 25 patient, expanded using standard tissue culture techniques, and returned to the patient.

 Alternatively, peptides corresponding to immunogenic portions of the polypeptides may be employed to generate tumor reactive T cell subsets by selective *in vitro* stimulation and expansion of autologous T cells to provide antigen-specific T cells which may be subsequently transferred to the patient as described, for example, by 30 Chang et al. (*Crit. Rev. Oncol. Hematol.*, 22(3), 213, 1996).

 In another embodiment, syngeneic or autologous dendritic cells may be pulsed with peptides corresponding to at least an immunogenic portion of a polypeptide

disclosed herein. The resulting antigen-specific dendritic cells may either be transferred into a patient, or employed to stimulate T cells to provide antigen-specific T cells which may, in turn, be administered to a patient. The use of peptide-pulsed dendritic cells to generate antigen-specific T cells and the subsequent use of such antigen-specific T cells 5 to eradicate tumors in a murine model has been demonstrated by Cheever et al. ("Therapy With Cultured T Cells: Principles Revisited," *Immunological Reviews*, 157:177, 1997).

Additionally vectors expressing the disclosed polynucleotides may be introduced into stem cells taken from the patient and clonally propagated *in vitro* for autologous 10 transplant back into the same patient. In one embodiment, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATETM system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated 15 with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

20 The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

25 EXAMPLE 1

PREPARATION OF BREAST TUMOR-SPECIFIC cDNAs USING DIFFERENTIAL DISPLAY RT-PCR

30 This Example illustrates the preparation of cDNA molecules encoding breast tumor-specific polypeptides using a differential display screen.

A. Preparation of B18Ag1 cDNA and Characterization of mRNA Expression

Tissue samples were prepared from breast tumor and normal tissue of a patient with breast cancer that was confirmed by pathology after removal from the patient. Normal RNA and tumor RNA was extracted from the samples and mRNA was isolated and converted into cDNA using a (dT)₁₂AG (SEQ ID NO:130) anchored 3' primer. Differential display PCR was then executed using a randomly chosen primer (CTTCAACCTC) (SEQ ID NO:103). Amplification conditions were standard buffer containing 1.5 mM MgCl₂, 20 pmol of primer, 500 pmol dNTP, and 1 unit of *Taq* DNA polymerase (Perkin-Elmer, Branchburg, NJ). Forty cycles of amplification were performed using 94°C denaturation for 30 seconds, 42°C annealing for 1 minute, and 72°C extension for 30 seconds. An RNA fingerprint containing 76 amplified products was obtained. Although the RNA fingerprint of breast tumor tissue was over 98% identical to that of the normal breast tissue, a band was repeatedly observed to be specific to the RNA fingerprint pattern of the tumor. This band was cut out of a silver stained gel, subcloned into the T-vector (Novagen, Madison, WI) and sequenced.

The sequence of the cDNA, referred to as B18Ag1, is provided in SEQ ID NO:1. A database search of GENBANK and EMBL revealed that the B18Ag1 fragment initially cloned is 77% identical to the endogenous human retroviral element S71, which is a truncated retroviral element homologous to the Simian Sarcoma Virus (SSV). S71 contains an incomplete *gag* gene, a portion of the *pol* gene and an LTR-like structure at the 3' terminus (see Werner et al., *Virology* 174:225-238 (1990)). B18Ag1 is also 64% identical to SSV in the region corresponding to the P30 (*gag*) locus. B18Ag1 contains three separate and incomplete reading frames covering a region which shares considerable homology to a wide variety of *gag* proteins of retroviruses which infect mammals. In addition, the homology to S71 is not just within the *gag* gene, but spans several kb of sequence including an LTR.

B18Ag1-specific PCR primers were synthesized using computer analysis guidelines. RT-PCR amplification (94°C, 30 seconds; 60°C → 42°C, 30 seconds; 72°C, 30 seconds for 40 cycles) confirmed that B18Ag1 represents an actual mRNA sequence present at relatively high levels in the patient's breast tumor tissue. The primers used in amplification were B18Ag1-1 (CTG CCT GAG CCA CAA ATG) (SEQ ID NO:128) and

B18Ag1-4 (CCG GAG GAG GAA GCT AGA GGA ATA) (SEQ ID NO:129) at a 3.5 mM magnesium concentration and a pH of 8.5, and B18Ag1-2 (ATG GCT ATT TTC GGG GCC TGA CA) (SEQ ID NO:126) and B18Ag1-3 (CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO:127) at 2 mM magnesium at pH 9.5. The same experiments 5 showed exceedingly low to nonexistent levels of expression in this patient's normal breast tissue (*see* Figure 1). RT-PCR experiments were then used to show that B18Ag1 mRNA is present in nine other breast tumor samples (from Brazilian and American patients) but absent in, or at exceedingly low levels in, the normal breast tissue corresponding to each cancer patient. RT-PCR analysis has also shown that the B18Ag1 10 transcript is not present in various normal tissues (including lymph node, myocardium and liver) and present at relatively low levels in PBMC and lung tissue. The presence of B18Ag1 mRNA in breast tumor samples, and its absence from normal breast tissue, has been confirmed by Northern blot analysis, as shown in Figure 2.

The differential expression of B18Ag1 in breast tumor tissue was also 15 confirmed by RNase protection assays. Figure 3 shows the level of B18Ag1 mRNA in various tissue types as determined in four different RNase protection assays. Lanes 1-12 represent various normal breast tissue samples, lanes 13-25 represent various breast tumor samples; lanes 26-27 represent normal prostate samples; lanes 28-29 represent prostate tumor samples; lanes 30-32 represent colon tumor samples; lane 33 represents 20 normal aorta; lane 34 represents normal small intestine; lane 35 represents normal skin, lane 36 represents normal lymph node; lane 37 represents normal ovary; lane 38 represents normal liver; lane 39 represents normal skeletal muscle; lane 40 represents a first normal stomach sample, lane 41 represents a second normal stomach sample; lane 42 represents a normal lung; lane 43 represents normal kidney; and lane 44 represents 25 normal pancreas. Interexperimental comparison was facilitated by including a positive control RNA of known β -actin message abundance in each assay and normalizing the results of the different assays with respect to this positive control.

RT-PCR and Southern Blot analysis has shown the B18Ag1 locus to be 30 present in human genomic DNA as a single copy endogenous retroviral element. A genomic clone of approximately 12-18 kb was isolated using the initial B18Ag1 sequence as a probe. Four additional subclones were also isolated by XbaI digestion.

Additional retroviral sequences obtained from the ends of the XbaI digests of these clones (located as shown in Figure 4) are shown as SEQ ID NO:3 - SEQ ID NO:10, where SEQ ID NO:3 shows the location of the sequence labeled 10 in Figure 4, SEQ ID NO:4 shows the location of the sequence labeled 11-29, SEQ ID NO:5 shows the 5 location of the sequence labeled 3, SEQ ID NO:6 shows the location of the sequence labeled 6, SEQ ID NO:7 shows the location of the sequence labeled 12, SEQ ID NO:8 shows the location of the sequence labeled 13, SEQ ID NO:9 shows the location of the sequence labeled 14 and SEQ ID NO:10 shows the location of the sequence labeled 11-22.

10 Subsequent studies demonstrated that the 12-18 kb genomic clone contains a retroviral element of about 7.75 kb, as shown in Figures 5A and 5B. The sequence of this retroviral element is shown in SEQ ID NO: 141. The numbered line at the top of Figure 5A represents the sense strand sequence of the retroviral genomic clone. The box below this line shows the position of selected restriction sites. The arrows 15 depict the different overlapping clones used to sequence the retroviral element. The direction of the arrow shows whether the single-pass subclone sequence corresponded to the sense or anti-sense strand. Figure 5B is a schematic diagram of the retroviral element containing B18Ag1 depicting the organization of viral genes within the element. The open boxes correspond to predicted reading frames, starting with a methionine, found 20 throughout the element. Each of the six likely reading frames is shown, as indicated to the left of the boxes, with frames 1-3 corresponding to those found on the sense strand.

Using the cDNA of SEQ ID NO:1 as a probe, a longer cDNA was obtained (SEQ ID NO:227) which contains minor nucleotide differences (less than 1%) compared to the genomic sequence shown in SEQ ID NO:141.

25 B. Preparation of cDNA Molecules Encoding Other Breast Tumor-Specific Polypeptides

Normal RNA and tumor RNA was prepared and mRNA was isolated and converted into cDNA using a (dT)₁₂AG anchored 3' primer, as described above. Differential display PCR was then executed using the randomly chosen primers of SEQ 30 ID NO: 87-125. Amplification conditions were as noted above, and bands observed to be specific to the RNA fingerprint pattern of the tumor were cut out of a silver stained

gel, subcloned into either the T-vector (Novagen, Madison, WI) or the pCRII vector (Invitrogen, San Diego, CA) and sequenced. The sequences are provided in SEQ ID NO:11 - SEQ ID NO:86. Of the 79 sequences isolated, 67 were found to be novel (SEQ ID NO:11-26 and 28-77) (*see also* Figures 6-20).

5 An extended DNA sequence (SEQ ID NO: 290) for the antigen B15Ag1 (originally identified partial sequence provided in SEQ ID NO: 27) was obtained in further studies. Comparison of the sequence of SEQ ID NO: 290 with those in the gene bank as described above, revealed homology to the known human β -A activin gene. Further studies led to the isolation of the full-length cDNA sequence for the antigen 10 B21GT2 (also referred to as B311D; originally identified partial cDNA sequence provided in SEQ ID NO: 56). The full-length sequence is provided in SEQ ID NO: 307, with the corresponding amino acid sequence being provided in SEQ ID NO: 308. Further studies led to the isolation of a splice variant of B311D. The B311D clone of 15 SEQ ID NO: 316 was sequenced and a XhoI/NotI fragment from this clone was gel purified and 32P-cDTP labeled by random priming for use as a probe for further screening to obtain additional B311D gene sequence. Two fractions of a human breast tumor cDNA bacterial library were screened using standard techniques. One of the clones isolated in this manner yielded additional sequence which includes a poly A+ tail. The determined cDNA sequence of this clone (referred to as B311D_BT1_1A) is 20 provided in SEQ ID NO: 317. The sequences of SEQ ID NO: 316 and 317 were found to share identity over a 464 bp region, with the sequences diverging near the poly A+ sequence of SEQ ID NO: 317.

Subsequent studies identified an additional 146 sequences (SEQ ID NOS:142-289), of which 115 appeared to be novel (SEQ ID NOS:142, 143, 146-152, 25 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288 and 291). To the best of the inventors' knowledge none of the previously identified sequences have heretofore been shown to be expressed at a greater level in human breast tumor tissue than in normal breast tissue.

30 In further studies, several different splice forms of the antigen B11Ag1 (also referred to as B305D) were isolated, with each of the various splice forms

containing slightly different versions of the B11Ag1 coding frame. Splice junction sequences define individual exons which, in various patterns and arrangements, make up the various splice forms. Primers were designed to examine the expression pattern of each of the exons using RT-PCR as described below. Each exon was found to show the same expression pattern as the original B11Ag1 clone, with expression being breast tumor-, normal prostate- and normal testis-specific. The determined cDNA sequences for the isolated protein coding exons are provided in SEQ ID NO: 292-298, respectively. The predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292 and 298 are provided in SEQ ID NO: 299 and 300. Additional studies using rapid amplification of cDNA ends (RACE), a 5' specific primer to one of the splice forms of B11Ag1 provided above and a breast adenocarcinoma, led to the isolation of three additional, related, splice forms referred to as isoforms B11C-15, B11C-8 and B11C-9,16. The determined cDNA sequences for these isoforms are provided in SEQ ID NO: 301-303, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 304-306.

In subsequent studies on B305D isoform A (cDNA sequence provided in SEQ ID NO: 292), the cDNA sequence (provided in SEQ ID NO: 313) was found to contain an additional guanine residue at position 884, leading to a frameshift in the open reading frame. The determined DNA sequence of this ORF is provided in SEQ ID NO: 314. This frameshift generates a protein sequence (provided in SEQ ID NO: 315) of 293 amino acids that contains the C-terminal domain common to the other isoforms of B305D but that differs in the N-terminal region.

EXAMPLE 2

25 PREPARATION OF B18AG1 DNA FROM HUMAN GENOMIC DNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human genomic DNA.

B18Ag1 DNA may be prepared from 250 ng human genomic DNA using 30 20 pmol of B18Ag1 specific primers, 500 pmol dNTPS and 1 unit of *Taq* DNA polymerase (Perkin Elmer, Branchburg, NJ) using the following amplification

parameters: 94°C for 30 seconds denaturing, 30 seconds 60°C to 42°C touchdown annealing in 2°C increments every two cycles and 72°C extension for 30 seconds. The last increment (a 42°C annealing temperature) should cycle 25 times. Primers were selected using computer analysis. Primers synthesized were B18Ag1-1, B18Ag1-2, 5 B18Ag1-3, and B18Ag1-4. Primer pairs that may be used are 1+3, 1+4, 2+3, and 2+4.

Following gel electrophoresis, the band corresponding to B18Ag1 DNA may be excised and cloned into a suitable vector.

EXAMPLE 3

10 PREPARATION OF B18Ag1 DNA FROM BREAST TUMOR cDNA

This Example illustrates the preparation of B18Ag1 DNA by amplification from human breast tumor cDNA.

First strand cDNA is synthesized from RNA prepared from human breast 15 tumor tissue in a reaction mixture containing 500 ng poly A+ RNA, 200 pmol of the primer (T)₁₂AG (*i.e.*, TTT TTT TTT TTT AG) (SEQ ID NO: 130), 1X first strand reverse transcriptase buffer, 6.7 mM DTT, 500 mmol dNTPs, and 1 unit AMV or MMLV reverse transcriptase (from any supplier, such as Gibco-BRL (Grand Island, NY)) in a final volume of 30 μ l. After first strand synthesis, the cDNA is diluted approximately 25 20 fold and 1 μ l is used for amplification as described in Example 2. While some primer pairs can result in a heterogeneous population of transcripts, the primers B18Ag1-2 (5'ATG GCT ATT TTC GGG GGC TGA CA) (SEQ ID NO: 126) and B18Ag1-3 (5'CCG GTA TCT CCT CGT GGG TAT T) (SEQ ID NO: 127) yield a single 151 bp amplification product.

25

EXAMPLE 4

IDENTIFICATION OF B-CELL AND T-CELL EPITOPES OF B18Ag1

This Example illustrates the identification of B18Ag1 epitopes.

30 The B18Ag1 sequence can be screened using a variety of computer algorithms. To determine B-cell epitopes, the sequence can be screened for

hydrophobicity and hydrophilicity values using the method of Hopp, *Prog. Clin. Biol. Res.* 172B:367-77 (1985) or, alternatively, Cease et al., *J. Exp. Med.* 164:1779-84 (1986) or Spouge et al., *J. Immunol.* 138:204-12 (1987). Additional Class II MHC (antibody or B-cell) epitopes can be predicted using programs such as AMPHI (e.g., Margalit et al., *J. Immunol.* 138:2213 (1987)) or the methods of Rothbard and Taylor (e.g., *EMBO J.* 7:93 (1988)).

Once peptides (15-20 amino acids long) are identified using these techniques, individual peptides can be synthesized using automated peptide synthesis equipment (available from manufacturers such as Perkin Elmer/Applied Biosystems 10 Division, Foster City, CA) and techniques such as Merrifield synthesis. Following synthesis, the peptides can be used to screen sera harvested from either normal or breast cancer patients to determine whether patients with breast cancer possess antibodies reactive with the peptides. Presence of such antibodies in breast cancer patient would confirm the immunogenicity of the specific B-cell epitope in question. The peptides can 15 also be tested for their ability to generate a serologic or humoral immune in animals (mice, rats, rabbits, chimps etc.) following immunization *in vivo*. Generation of a peptide-specific antiserum following such immunization further confirms the immunogenicity of the specific B-cell epitope in question.

To identify T-cell epitopes, the B18Ag1 sequence can be screened using 20 different computer algorithms which are useful in identifying 8-10 amino acid motifs within the B18Ag1 sequence which are capable of binding to HLA Class I MHC molecules. (see, e.g., Rammensee et al., *Immunogenetics* 41:178-228 (1995)). Following synthesis such peptides can be tested for their ability to bind to class I MHC using standard binding assays (e.g., Sette et al., *J. Immunol.* 153:5586-92 (1994)) and more 25 importantly can be tested for their ability to generate antigen reactive cytotoxic T-cells following *in vitro* stimulation of patient or normal peripheral mononuclear cells using, for example, the methods of Bakker et al., *Cancer Res.* 55:5330-34 (1995); Visseren et al., *J. Immunol.* 154:3991-98 (1995); Kawakami et al., *J. Immunol.* 154:3961-68 (1995); and Kast et al., *J. Immunol.* 152:3904-12 (1994). Successful *in vitro* generation of T- 30 cells capable of killing autologous (bearing the same Class I MHC molecules) tumor cells following *in vitro* peptide stimulation further confirms the immunogenicity of the

B18Ag1 antigen. Furthermore, such peptides may be used to generate murine peptide and B18Ag1 reactive cytotoxic T-cells following *in vivo* immunization in mice rendered transgenic for expression of a particular human MHC Class I haplotype (Vitiello et al., *J. Exp. Med.* 173:1007-15 (1991)).

5 A representative list of predicted B18Ag1 B-cell and T-cell epitopes, broken down according to predicted HLA Class I MHC binding antigen, is shown below:

Predicted Th Motifs (B-cell epitopes) (SEQ ID NOS.: 131-133)

SSGGRTFDDFHRYLLVGI
10 QGAAQKPINLSKXIEVVQGHDE
SPGVFLEHLQEAYRIYTPFDLSA

Predicted HLA A2.1 Motifs (T-cell epitopes) (SEQ ID NOS.: 134-140)

15 YLLVGIQGA
GAAQKPINL
NLSKXIEVV
EVVQGHDES
HLQEAYRIY
NLAFAAQAA
20 FVAQAAAPDS

EXAMPLE 5

IDENTIFICATION OF T-CELL EPITOPES OF B11Ag1

This Example illustrates the identification of B11Ag1 (also referred to as
25 B305D) epitopes. Four peptides, referred to as B11-8, B11-1, B11-5 and B11-12 (SEQ
ID NO: 309-312, respectfully) were derived from the B11Ag1 gene.

Human CD8 T cells were primed *in vitro* to the peptide B11-8 using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8 T cell cultures were tested for their 30 ability to recognize the B11-8 peptide or a negative control peptide, presented by the B-LCL line, JY. Briefly, T cells were incubated with autologous monocytes in the presence

of 10 ug/ml peptide, 10 ng/ml IL-7 and 10 ug/ml IL-2, and assayed for their ability to specifically lyse target cells in a standard 51-Cr release assay. As shown in Fig. 22, the bulk culture line demonstrated strong recognition of the B11-8 peptide with weaker recognition of the peptide B11-1.

5 A clone from this CTL line was isolated following rapid expansion using the monoclonal antibody OKT3 and human IL-2. As shown in Fig. 23, this clone (referred to as A1), in addition to being able to recognize specific peptide, recognized JY LCL transduced with the B11Ag1 gene. This data demonstrates that B11-8 is a naturally processed epitope of the B11Ag1 gene. In addition these T cells were further found to 10 recognize and lyse, in an HLA-A2 restricted manner, an established tumor cell line naturally expressing B11Ag1 (Fig. 24). The T cells strongly recognize a lung adenocarcinoma (LT-140-22) naturally expressing B11Ag1 transduced with HLA-A2, as well as an A2+ breast carcinoma (CAMA-1) transduced with B11Ag1, but not untransduced lines or another negative tumor line (SW620).

15 These data clearly demonstrate that these human T cells recognize not only B11-specific peptides but also transduced cells, as well as naturally expressing tumor lines.

20 CTL lines raised against the antigens B11-5 and B11-12, using the procedures described above, were found to recognize corresponding peptide-coated targets.

Example 6

CHARACTERIZATION OF BREAST TUMOR GENES DISCOVERED BY
DIFFERENTIAL DISPLAY PCR

5 The specificity and sensitivity of the breast tumor genes discovered by differential display PCR were determined using RT-PCR. This procedure enabled the rapid evaluation of breast tumor gene mRNA expression semiquantitatively without using large amounts of RNA. Using gene specific primers, mRNA expression levels in a variety of tissues were examined, including 8 breast tumors, 5 normal breasts, 2 prostate
10 tumors, 2 colon tumors, 1 lung tumor, and 14 other normal adult human tissues, including normal prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach and testes.

To ensure the semiquantitative nature of the RT-PCR, β -actin was used as internal control for each of the tissues examined. Serial dilutions of the first strand
15 cDNAs were prepared and RT-PCR assays performed using β -actin specific primers. A dilution was then selected that enabled the linear range amplification of β -actin template, and which was sensitive enough to reflect the difference in the initial copy number. Using this condition, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and
20 by assuring a negative result when using first strand cDNA that was prepared without adding reverse transcriptase.

Using gene specific primers, the mRNA expression levels were determined in a variety of tissues. To date, 38 genes have been successfully examined by RT-PCR, five of which exhibit good specificity and sensitivity for breast tumors
25 (B15AG-1, B31GA1b, B38GA2a, B11A1a and B18AG1a). Figures 21A and 21B depict the results for three of these genes: B15AG-1 (SEQ ID NO:27), B31GA1b (SEQ ID NO:148) and B38GA2a (SEQ ID NO. 157). Table I summarizes the expression level of all the genes tested in normal breast tissue and breast tumors, and also in other tissues.

TABLE I

Percentage of Breast Cancer Antigens that are Expressed in Various Tissues

5	Breast Tissues	Over-expressed in Breast Tumors	84%
		Equally Expressed in Normals and Tumor	16%
10		Over-expressed in Breast Tumors but not in any Normal Tissues	9%
15	Other Tissues	Over-expressed in Breast Tumors but Expressed in Some Normal Tissues	30%
		Over-expressed in Breast Tumors but Equally Expressed in All Other Tissues	61%
20		From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.	

CLAIMS

1. An isolated polypeptide, comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

(c) complements of sequences of (a) or (b).

20

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences.

30

3. An isolated polypeptide comprising a sequence recited in any

one of SEQ ID NOs: 299, 300, 304-306, 308 and 315.

4. An isolated polynucleotide encoding at least 15 amino acid residues of a protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein 5 comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement 10 of any of the foregoing sequences.

5. An isolated polynucleotide encoding a protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs: 1, 3-15 26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing sequences.

20 6. An isolated polynucleotide, comprising a sequence recited in any one of SEQ ID Nos: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

25

7. An isolated polynucleotide, comprising a sequence that hybridizes to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 30 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317

under moderately stringent conditions.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

5

9. An expression vector, comprising a polynucleotide according to any one of claims 4-8.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences.

20 12. A fusion protein, comprising at least one polypeptide according to claim 1.

25 13. A fusion protein according to claim 12, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

14. A fusion protein according to claim 12, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

15. A fusion protein according to claim 12, wherein the fusion protein comprises an affinity tag.

16. An isolated polynucleotide encoding a fusion protein according
5 to claim 12.

17. A pharmaceutical composition, comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- 10 (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

15 18. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:

- (a) a polypeptide according to claim 1;
- (b) a polynucleotide according to claim 4;
- (c) an antibody according to claim 11;
- 20 (d) a fusion protein according to claim 12; and
- (e) a polynucleotide according to claim 16.

19. A vaccine according to claim 18, wherein the immunostimulant is an adjuvant.

25

20. A vaccine according to any claim 18, wherein the immunostimulant induces a predominantly Type I response.

21. A method for inhibiting the development of a cancer in a
30 patient, comprising administering to a patient an effective amount of a pharmaceutical

composition according to claim 17.

22. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine
5 according to claim 18.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

10

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. A vaccine comprising an antigen-presenting cell that expresses
15 a polypeptide comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NOS: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

20 (b) sequences that hybridize to a sequence recited in any one of SEQ ID NOS: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

(c) complements of sequences of (i) or (ii);
in combination with an immunostimulant.

25

26. A vaccine according to claim 25, wherein the immunostimulant is an adjuvant.

27. A vaccine according to claim 25, wherein the immunostimulant
30 induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

5 29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group
10 consisting of:

(a) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

(b) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317

15 under moderately stringent conditions; and

(c) complements of sequences encoded by a polynucleotide recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

and thereby inhibiting the development of a cancer in the patient.

20

30. A method according to claim 29, wherein the antigen-presenting cell is a dendritic cell.

31. A method according to any one of claims 21, 22 and 29,
25 wherein the cancer is breast cancer.

32. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a protein, wherein the protein comprises an amino acid sequence that is encoded by a
30 polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317; and
(ii) complements of the foregoing polynucleotides;
wherein the step of contacting is performed under conditions and for a
5 time sufficient to permit the removal of cells expressing the antigen from the sample.

33. A method according to claim 32, wherein the biological sample is blood or a fraction thereof.

10 34. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 32.

15 35. A method for stimulating and/or expanding T cells specific for a protein, comprising contacting T cells with at least one component selected from the group consisting of:

20 (a) polypeptides comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:
(i) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;
(ii) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and
25 (iii) complements of sequences of (i) or (ii);
(b) polynucleotides encoding a polypeptide of (a); and
(c) antigen presenting cells that express a polypeptide of (a);
under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

36. An isolated T cell population, comprising T cells prepared according to the method of claim 35.

37. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 36.

38. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

10 (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

15 (i) polypeptides comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

20 (1) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

(2) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

(3) complements of sequences of (1) or (2);

(ii) polynucleotides encoding a polypeptide of (i); and

(iii) antigen presenting cells that expresses a polypeptide of (i);

25 such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

39. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) polypeptides comprising at least an immunogenic portion of a protein, or a variant thereof, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(1) sequences recited in SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317;

(2) sequences that hybridize to a sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 under moderately stringent conditions; and

(3) complements of sequences of (1) or (2);

(ii) polynucleotides encoding a polypeptide of (i); and

(iii) antigen presenting cells that express a

15 polypeptide of (i);

such that T cells proliferate;

(b) cloning at least one proliferated cell to provide cloned T cells;

and

20 (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

40. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with a binding agent that binds to a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

5 41. A method according to claim 40, wherein the binding agent is an antibody.

42. A method according to claim 43, wherein the antibody is a monoclonal antibody.

10

43. A method according to claim 40, wherein the cancer is breast cancer.

44. A method for monitoring the progression of a cancer in a 15 patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOS: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 20 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b) using a biological sample obtained 25 from the patient at a subsequent point in time; and

(d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

30 45. A method according to claim 44, wherein the binding agent is

an antibody.

46. A method according to claim 45, wherein the antibody is a monoclonal antibody.

5

47. A method according to claim 44, wherein the cancer is a breast cancer.

48. A method for determining the presence or absence of a cancer 10 in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1, 3-26, 28-86, 142-253, 255-298, 301-15 303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the 20 oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

49. A method according to claim 48, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a 25 polymerase chain reaction.

50. A method according to claim 48, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

51. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

- (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NO: 1, 3-26, 28-86, 142-253, 255-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotide sequences;
- (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;
- (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

52. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

20

53. A method according to claim 51, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

25

54. A diagnostic kit, comprising:

- (a) one or more antibodies according to claim 11; and
- (b) a detection reagent comprising a reporter group.

30

55. A kit according to claim 54, wherein the antibodies are

immobilized on a solid support.

56. A kit according to claim 54, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

5 57. A kit according to claim 54, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

10 58. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a protein, wherein the protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOS: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 15 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317 or a complement of any of the foregoing polynucleotides.

20 59. A oligonucleotide according to claim 58, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID Nos: 1, 3-26, 28-77, 142, 143, 146-152, 154-166, 168-176, 178-192, 194-198, 200-204, 206, 207, 209-214, 216, 218, 219, 221-240, 243-245, 247, 250, 251, 253, 255, 257-266, 268, 269, 271-273, 275, 276, 278, 280, 281, 284, 288, 291-298, 301-303, 307, 313, 314, 316 and 317.

25 60. A diagnostic kit, comprising:
(a) an oligonucleotide according to claim 59; and
(b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

COMPOSITIONS AND METHODS FOR THE TREATMENT
AND DIAGNOSIS OF BREAST CANCER

5

ABSTRACT OF THE DISCLOSURE

Compositions and methods for the detection and therapy of breast
10 cancer are disclosed. The compounds provided include nucleotide sequences that are
preferentially expressed in breast tumor tissue, as well as polypeptides encoded by
such nucleotide sequences. Vaccines and pharmaceutical compositions comprising
such compounds are also provided and may be used, for example, for the prevention
and treatment of breast cancer. The polypeptides may also be used for the production
15 of antibodies, which are useful for diagnosing and monitoring the progression of
breast cancer in a patient.

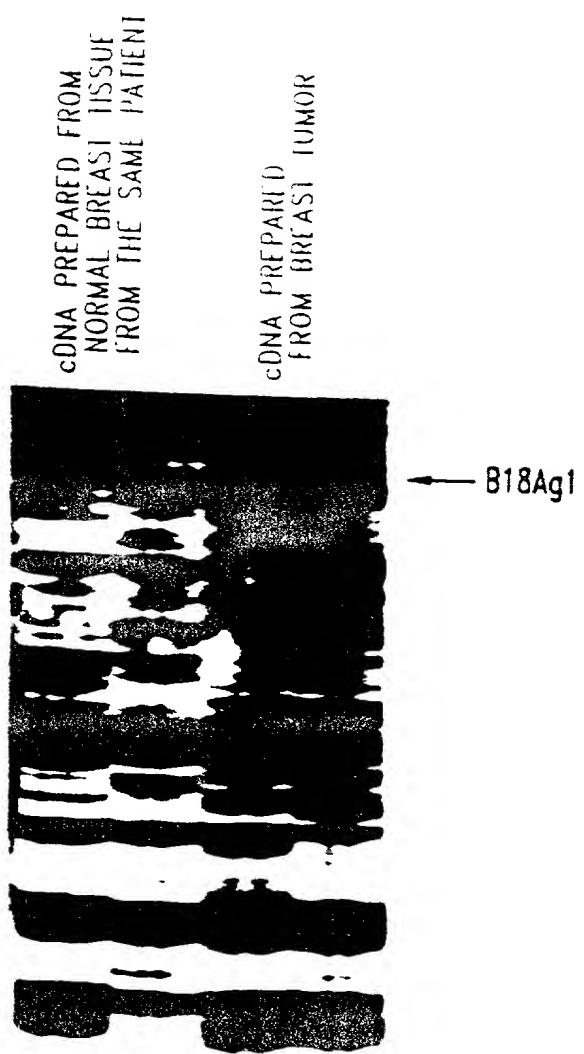


Fig. 1

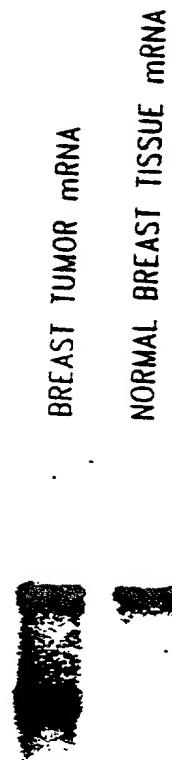


Fig. 2

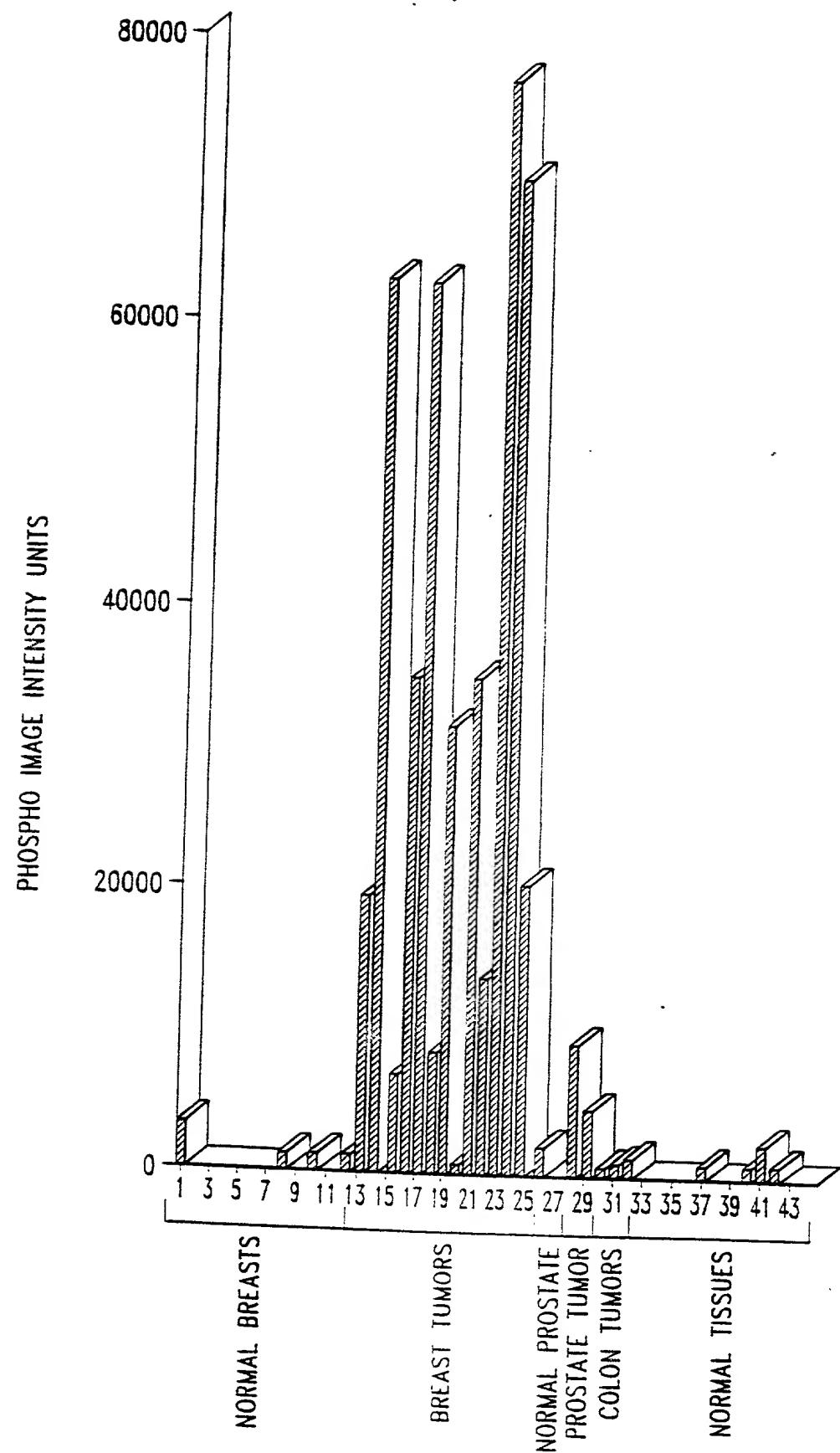


Fig. 3

GENOMIC CLONE MAP

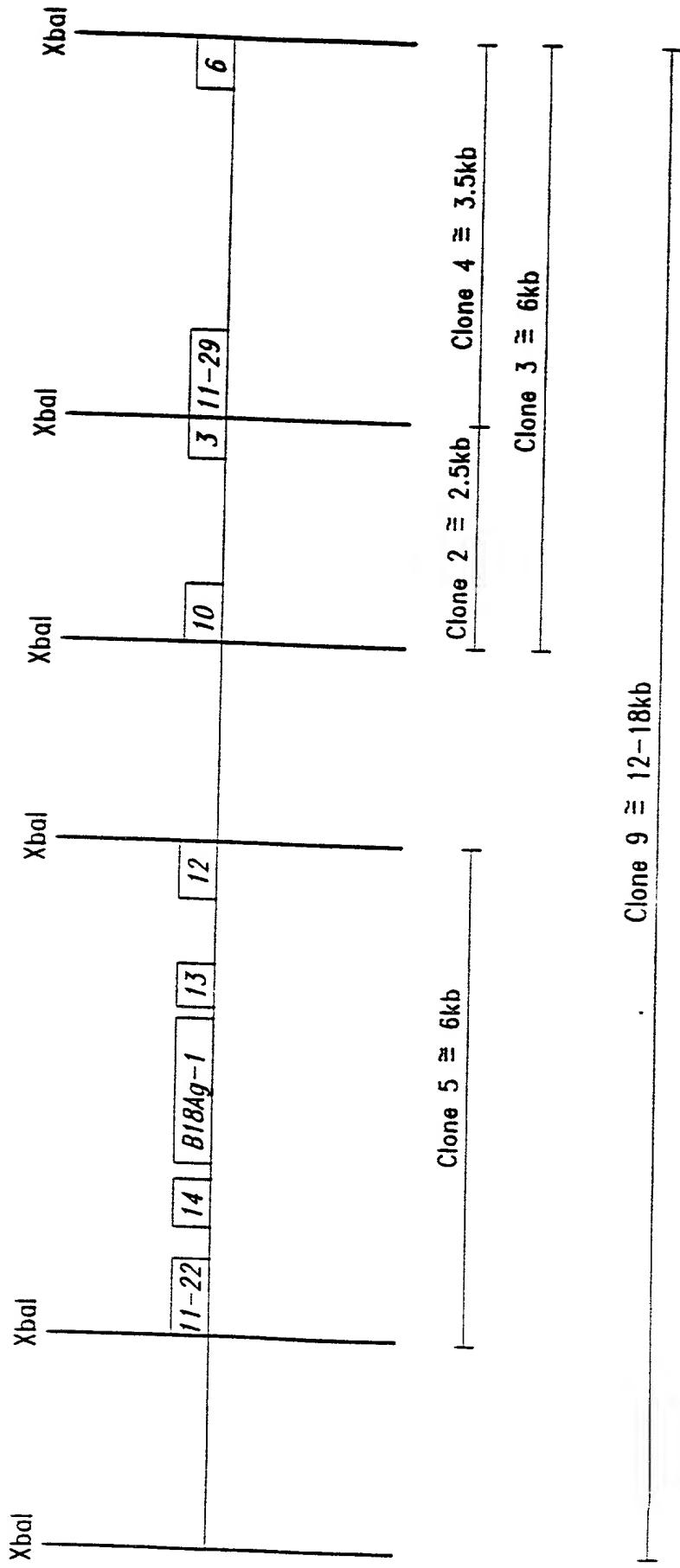


Fig. 4

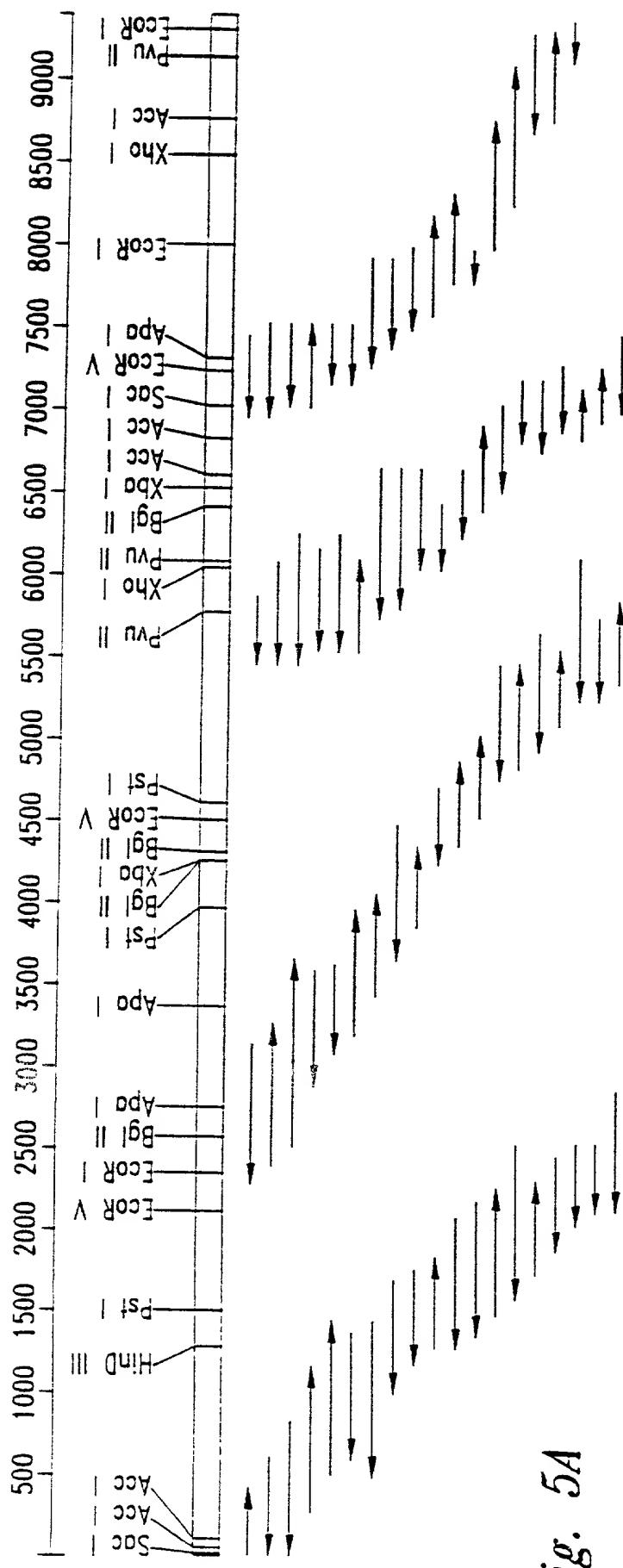


Fig. 5A

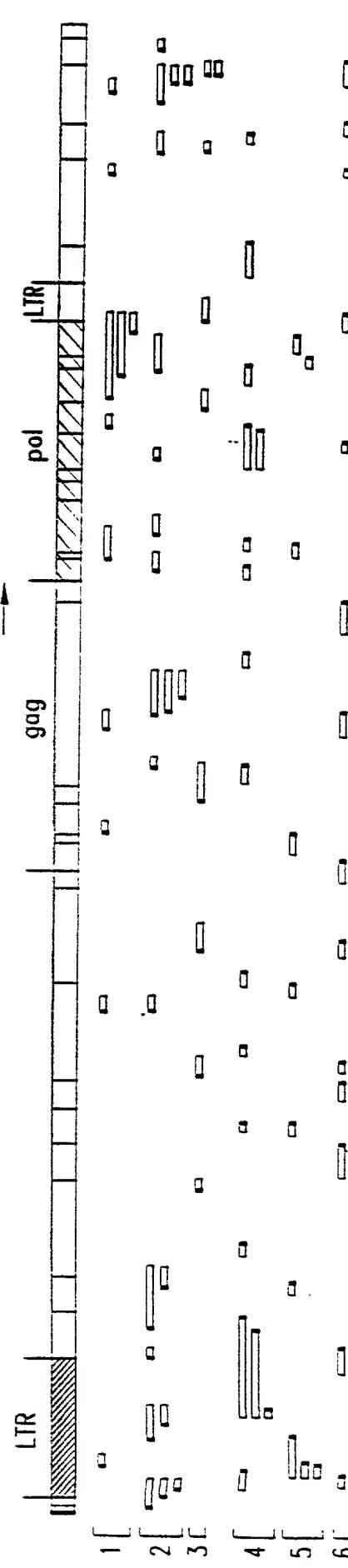


Fig. 5B

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B18Ag1

TTA GAG ACC CAA TTG GGA CCT AAT TGG GAC CCA AAT TTC TCA AGT GGA	48
Leu Glu Thr Gln Leu Gly Pro Asn Trp Asp Pro Asn Phe Ser Ser Gly	
1 5 10 15	
GGG AGA ACT TTT GAC GAT TTC CAC CGG TAT CTC CTC GTG GGT ATT CAG	96
Gly Arg Thr Phe Asp Asp Phe His Arg Tyr Leu Leu Val Gly Ile Gln	
20 25 30	
GGA GCT GCC CAG AAA CCT ATA AAC TTG TCT AAG GCG ATT GAA GTC GTC	144
Gly Ala Ala Gln Lys Pro Ile Asn Leu Ser Lys Ala Ile Glu Val Val	
35 40 45	
CAG GGG CAT GAT GAG TCA CCA GGA GTG TTT TTA GAG CAC CTC CAG GAG	192
Gln Gly His Asp Glu Ser Pro Gly Val Phe Leu Glu His Leu Gln Glu	
50 55 60	
GCT TAT CGG ATT TAC ACC CCT TTT GAC CTG GCA GCC CCC GAA AAT AGC	240
Ala Tyr Arg Ile Tyr Thr Pro Phe Asp Leu Ala Ala Pro Glu Asn Ser	
65 70 75 80	
CAT GCT CTT AAT TTG GCA TTT GTG GCT CAG GCA GCC CCA GAT AGT AAA	288
His Ala Leu Asn Leu Ala Phe Val Ala Gln Ala Ala Pro Asp Ser Lys	
85 90 95	
AGG AAA CTC CAA AAA CTA GAG GGA TTT TGC TGG AAT GAA TAC CAG TCA	336
Arg Lys Leu Gln Lys Leu Glu Gly Phe Cys Trp Asn Glu Tyr Gln Ser	
100 105 110	
GCT TTT AGA GAT AGC CTA AAA GGT TTT	363
Ala Phe Arg Asp Ser Leu Lys Gly Phe	
115 120	

Fig. 6

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA 817Ag1

GC TGGGCACAGT GGCTCATACC TGTAAATCCTG ACCGTTTCAG AGGCTCAGGT	60
CG CTTGAGCCCCA AGATTTCAAG ACTAGTCTGG GTAACATAGT GAGACCCAT	120
AA AAATAAAAAAA ATGAGGCCTGG TGTAGTGGCA CACACCAAGCT GAGGAGGGAG	180
CT AGGAGA	196

Fig. 7

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B17Ag2

GC TTGGGGGCTC TGACTAGAAA TTCAAGGAAC CTGGGATTCA AGTCCAAGT	60
AC TTACACTGTG GNCTCCAATA AACTGCTTCT TTCTTATTCC CTCTCTATTA	120
AA GGAAAACGAT GTCTGTGTAT AGCCAAGTCA GNTATCCTAA AAGGAGATAC	180
AT TAAATATCAG AATGTAAAAC CTGGGAACCA GGTTCCCAGC CTGGGATTAA	240
CA AGAAGACTGA ACAGTACTAC TGTGAAAAGC CCGAAGNGGC AATATGTTCA	300
TT GAAGGATGGC TGGGAGAATG AATGCTCTGT CCCCCAGTCC CAAGCTCACT	360
CT CCTTTATAGC CTAGGAGA	388

Fig. 8

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag2a

GC CTATAATCAT GTTTCTCATT ATTTTCACAT TTTATTAACC AATTTCTGTT	60
AA AATATGAGGG AAATATATGA AACAGGGAGG CAATGTTCAAG ATAATTGATC	120
TG ATTTCTACAT CAGATGCTCT TTCCCTTCCT GTTTATTCCT TTTTTATTC	180
GG TCGAATGTAA TAGCTTGTT TCAAGAGAGA GTTTGGCAG TTTCTGTAGC	240
CT GCTCATGTCT CCAGGCATCT ATTTGCACTT TAGGAGGTGT CGTGGGAGAC	300
CT ATTTTTCCA TATTTGGCA ACTACTA	337

Fig. 9

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1b

GC CATACTAGTGC CTTTCCATT ATTAAACCCC CACCTGAACG GCATAAACTG	60
GC TGGTGTAAAA TACTGTAAC AATAAGGAGA CTTTGCTCTT CATTAAACC	120
AT TTCATATTTT ACGCTCGAGG GTTTTACCG GTTCCTTTT ACACTCCTTA	180
TT TAAGTCGTTT GGAACAAGAT ATTTTTCTT TCCTGGCAGC TTTAACATT	240
TT TGTGTCTGGG GGACTGCTGC TCACTGTTTC TCACAGTTCC AAATCAAGGC	300
CC AAGAAAAAAA AATTTTTTG TTTTATTTGA AACTGGACCG GATAAACGGT	360
CG GCTGCTGTAT ATAGTTTAA ATGGTTATT GCACCTCCTT AAGTTGCACT	420
GG GGGGNTTTTG NATAGAAAGT NTTTANTCAC ANAGTCACAG GGACTTTNT	480
NA CTGAGCTAAA AAGGGCTGNT TTTCGGGTGG GGGCAGATGA AGGCTCACAG	540
TC TCTTAGAGGG GGGAACTNCT A	571

Fig. 10

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B13Ag1a

TA ATAACCTAAA TATATTTGA TCACCCACTG GGGTGATAAG ACAATAGATA	60
TT TCCAAAAAGC ATAAAACCAA AGTATCATAC CAAACCAAAT TCATACTGCT	120
CC GCACTGAAAC TTCACCTTCT AACTGTCTAC CTAACCAAAT TCTACCCCTTC	180
GG TGCCTGCTCA CTACTCTTTT TTTTTTTTTT TTTNTTTGG AGATGGAGTC	240
CA GCCCAGGGGT GGAGTACAAT GGCACAAACCT CAGCTCACTG NAACCTCCGC	300
TT CATGAGATTG TCCTGNTTCA GCCTTCCCAG TAGCTGGGAC TACAGGTGTG	360
TG CCTGGNTAAT CTTTTTNGT TTTNGGGTAG AGATGGGGGT TTTACATGTT	420
TG GTNTCGAACT CCTGACCTCA AGTGATCCAC CCACCTCAGG CTCCCAAAGT	480
TA CAGACATGAG CCACTGNGCC CAGNCCTGGT GCATGCTCAC TTCTCTAGGC	540
	548

Fig. 11

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B11Ag1

TG CACATGCAGA ATATTCTATC GGTACTTCAG CTATTACTCA TTTTGATGGC	60
AG CCTATCCTCA AGATGAGTAT TTAGAAAGAA TTGATTTAGC GATAGACCAA	120
GC ACTCTGACTA CACGAAATTG TTCAGATGTG ATGGATTAT GACAGTTGAT	180
GA GATTATTAAG TGATTATTT AAAGGGAATC CATTAAATTCC AGAATATCTT	240
TC AAGATGATAT AGAAATAGAA CAGAAAGAGA CTACAAATGA AGATGTATCA	300
TA TTGAAGAGCC TATAGTAGAA AATGAATTAG CTGCATTTAT TAGCCTTACA	360
TT TTCCTGATGA ATCTTATATT CAGCCATCGA CATAGCATT A CCTGATGGC	420
GA ATAATAGAAA CTGGGTGCGG GGCTATTGAT GAATTCACTCC NCAGTAAATT	480
AC AAAATATAAC TCGATTGCAT TTGGATGATG GAATACTAAA TCTGGCAAAA	540
GG AGCTACTAGT AACCTCTCTT TTTGAGATGC AAAATTTCT TT-TAGGGTTT	600
CT ACTTTACGGA TATTGGAGCA TAACGGGA	638

Fig. 12

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA3c

ACTGATGGAT GTCGCCGGAG GCGAGGGGCC TTATCTGATG CTCGGCTGCC TGTTCGTGAT 60
·GTGCGCGGGCG ATTGGGCTGT TTATCTCAAA CACCGCCACG GCGGTGCTGA TGGCGCCTAT 120
TGCCTTAGCG GCGGCGAAGT CAATGGCGT CTCACCCAT CCTTTGCCA TGGTGGTGGC 180
GATGGCGGCT TCGGCGGCGT TTATGACCCC GGTCTCCTCG CGGGTTAACAA CCTGGTGCT 240
TGGCCCTGGC AAGTACTCAT TTAGCGATT TGTCAAAATA GGCGTG 286

Fig. 13

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG1

AG CAGCCCCTTC TTCTCAATT CATCTGTACAC TACCCCTGGTG TAGTATCTCA	60
CA TTTTATAGC CTCCCTCCCTG GTCTGTCTTT TGATTTCCCT GCCTGTAATC	120
AC ATAACGTCAA GTAAACATTT CTAAAGTGTG GTTATGCTCA TGTCACTCCT	180
AA ATAGTTCCA TTACCGTCTT AATAAAATTG GGATTTGTTTC TTTNCTATTN	240
CA CCTATGACCG AA	262

Fig. 14

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B9CG3

AG CAAAGCCAGT GGTTTGAGCT CTCTACTGTG TAAACTCCTA AACCAAGGCC	60
TA AATGGTGGCA GGATTTTAT TATAAACATG TACCCATGCA AATTCCTAT	120
GA TATATTCTTC TACATTTAAA CAATAAAAAT AATCTATTT TAAAAGCCTA	180
AG TTAGGTAAGA GTGTTAATG AGAGGGTATA AGGTATAAAAT CACCAAGTCAA	240
TG CCTATGACCG A	261

Fig. 15

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B2CA2

GG GCATGGACGC AGACGCCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTCTG	60
AT AGGAAAATTC CCAAAGAGGG AATGTCTGT TGCTGCCAG TTTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCTTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 16

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA1

GG GCATGGACGC AGACGCCCTGA CGTTTGGCTG AAAATCTTTC ATTGATTGTT	60
AT AGGAAAATTC CCAAAGAGGG AATGTCCTGT TGCTGCCAG TTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGNN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 17

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA2

GG GCATGGACGC AGACGCCTGA CGTTGGCTG AAAATCTTC ATTGATTG	60
AT AGGAAAATTC CCAAAGAGGG AATGTCTGT TGCTGCCAG TTTTNTGTT	120
GG ANAAGGCAAN GAGCTCTTCA GACTATTGGN ATTNTCGTTC GGTCTTCTGC	180
CG NCTTGCNANG ATCTTCAT	208

Fig. 18

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B3CA3

AG GGAGCAAGGA	GAAGGCATGG	AGAGGGCTCAN	GCTGGTCCTG	GCCTACGACT	60
CT GTCGCCGGGG	ATGGTGGAGA	ACTGAAGCGG	GACCTCCTCG	AGGTCCCTCCG	120
TC NCCGTCCAGG	AGGAGGGTCT	TTCCCGTGGTC	TNGGAGGAGC	GGGGGGAGAA	180
TC ATGGTCNACA	TCCC				204

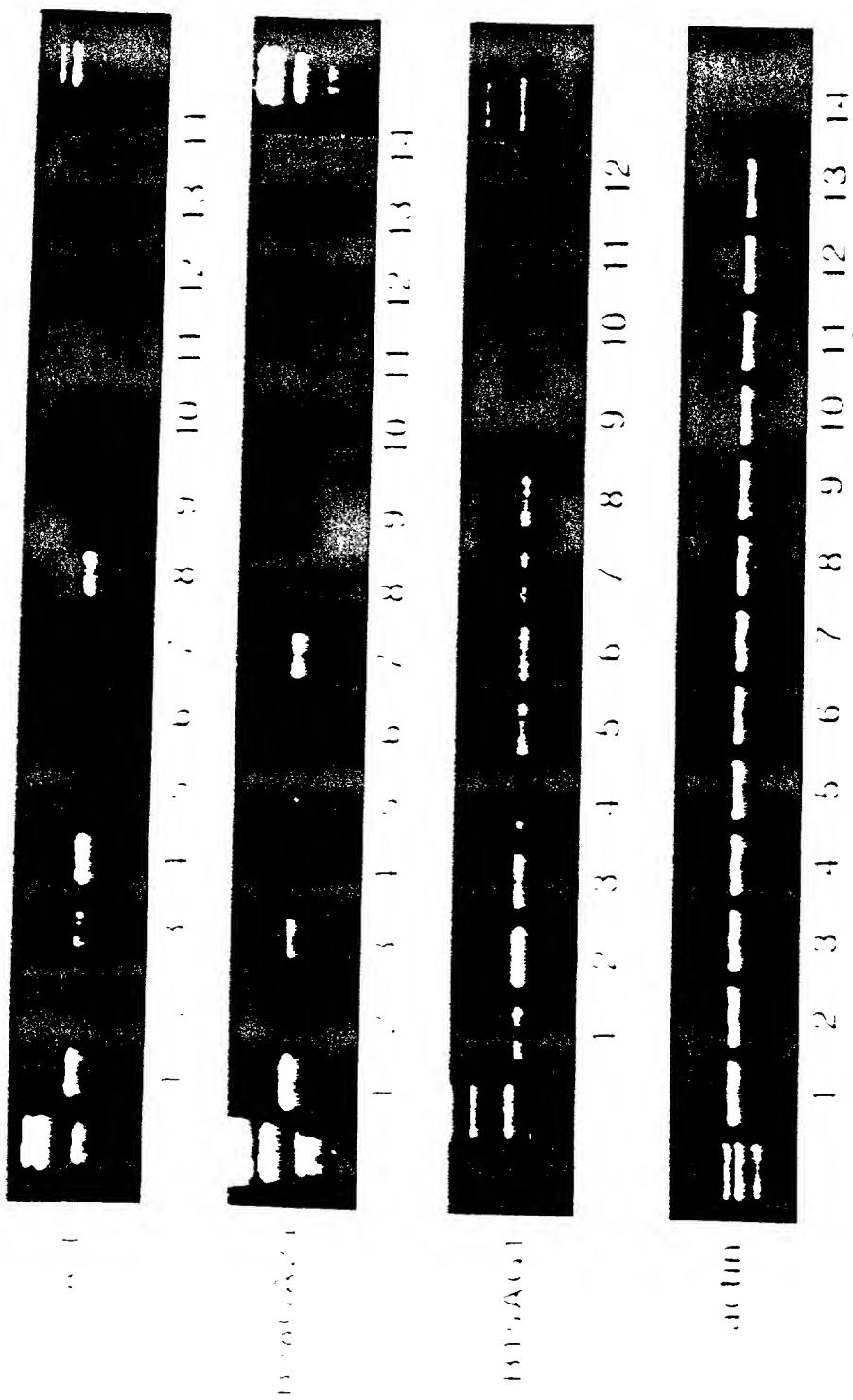
Fig. 19

NUCLEOTIDE SEQUENCE OF THE REPRESENTATIVE
BREAST-TUMOR SPECIFIC cDNA B4CA1

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TG ATAGTTGCTG AGTTTTCTT TGACCCATGA GTTATATTGG AGTTTATTTT	120
CC AATCGCATGG ACATGTTAGA CTTATTTCT GTTAATGATT NCTATTTTA	180
GA TTTGAGAAAT TGGTTNTTAT TATATCAATT TTTGGTATT GTTGAGTTG	240
GC TTAGTATGTG ACCA	264

Fig. 20

Fig. 21A



B31(A1)



B30(A1)



B15(A1)



b) achen

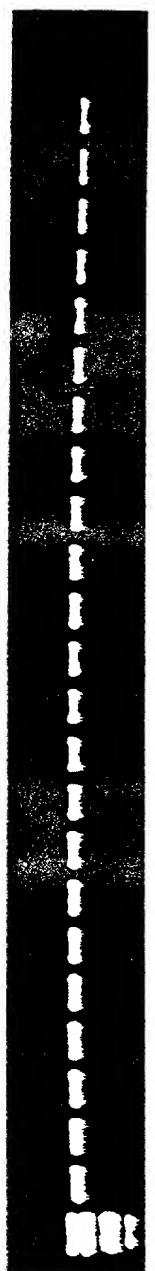


Fig. 21B

Recognition of Peptide by D142 anti-B11-8 CTL line

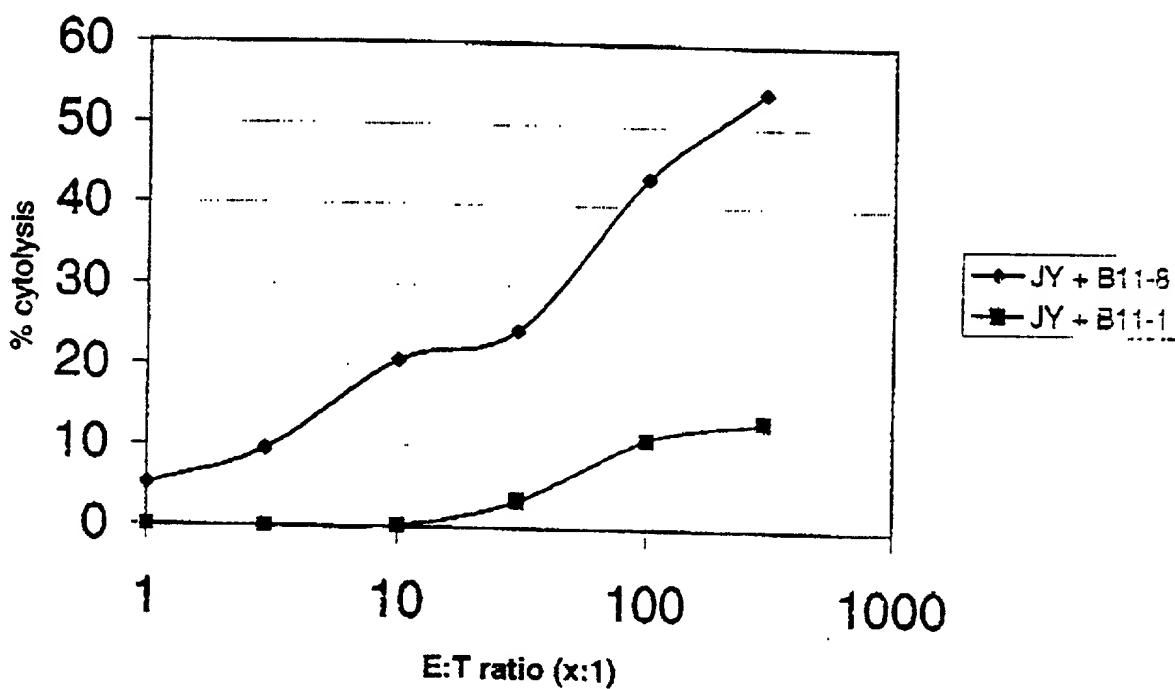


Fig. 22

Recognition of B11 Transductant by B11-8 Specific Clone A1

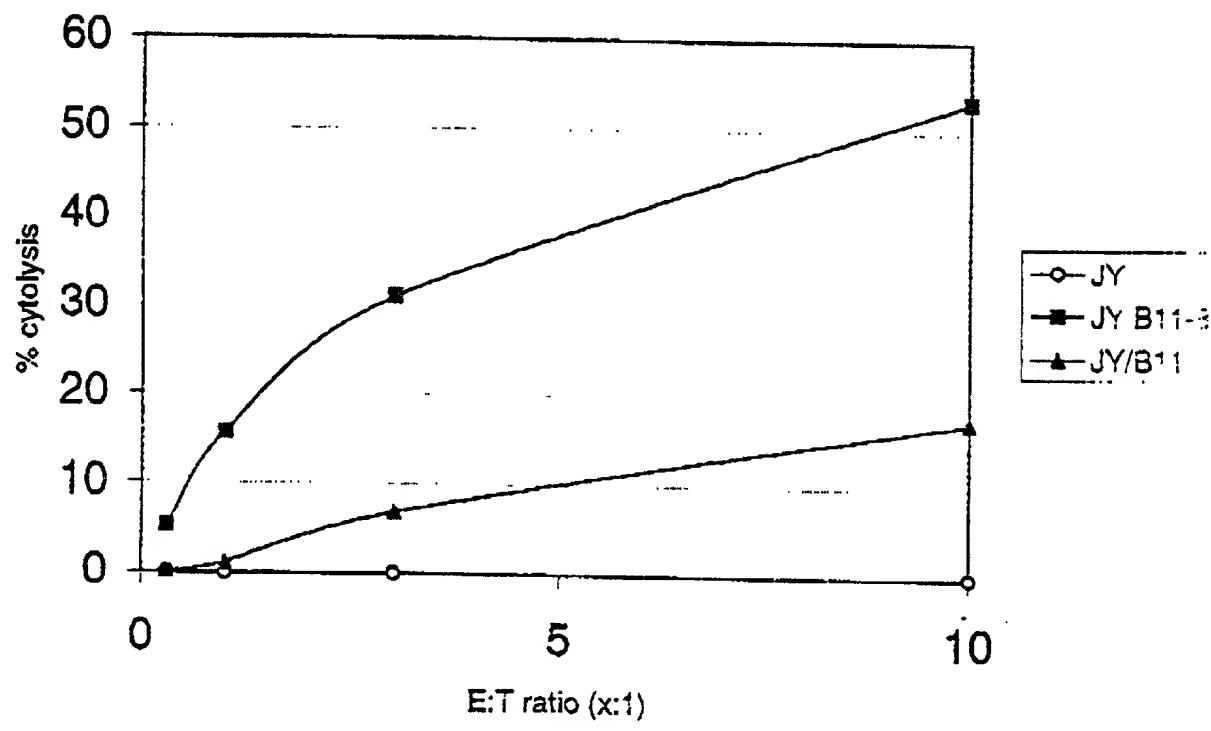


Fig. 23

Recognition of Tumor Cell Lines by Clone A1

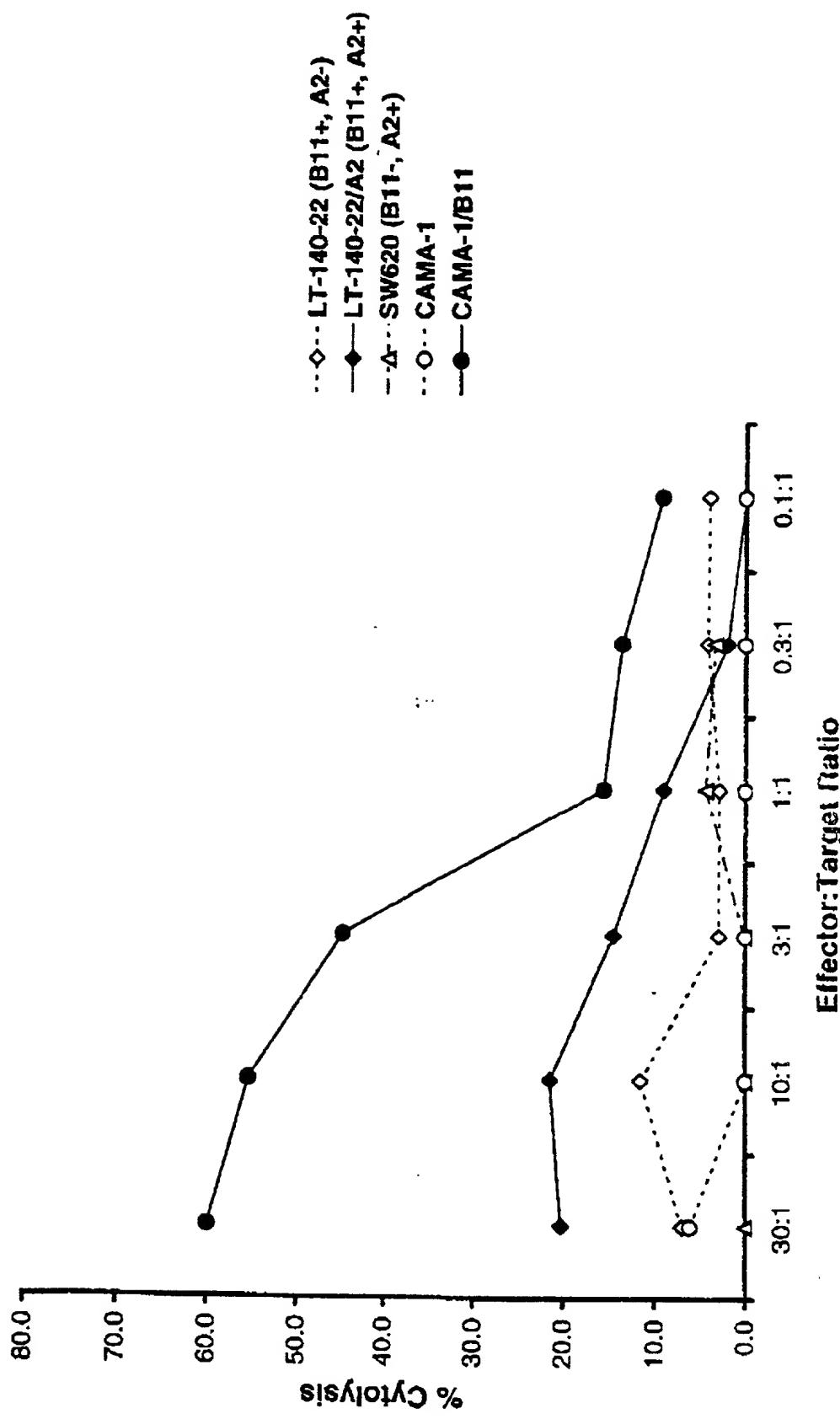


Fig. 24

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Tony N. Frudakis, John M. Smith, Steven G. Reed, Lynda E. Misher
Marc W. Retter and Davin C. Dillon.

Filed : March 23, 2000

For : COMPOSITIONS AND METHODS FOR THE TREATMENT AND
DIAGNOSIS OF BREAST CANCER

Docket No. : 210121.419C7

Date : March 23, 2000

Box Patent Application
Assistant Commissioner for Patents
Washington, D.C. 20231

DECLARATION

Sir:

I, Monica Steinborn, in accordance with 37 C.F.R. § 1.821(f) do hereby declare that, to the best of my knowledge, the content of the paper entitled "Sequence Listing" and the computer readable copy contained within the floppy disk are the same.

I declare further that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated this 23rd day of March, 2000.

Monica Steinborn
Monica Steinborn
Legal Assistant

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Seattle, WA 98104-7092
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FAX (206) 682-6031

SEQUENCE LISTING

<110> Frudakis, Tony N.
Smith, John M.
Reed, Steven G.
Misher, Lynda
Retter, Marc W.
Dillon, Davin C.

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gaagccggga	atttcattaa	caacccgcca	cacagctga	acattgtgag	gttcagtgac	660
cottcaaggg	gccactccac	tccaactttg	gccattctac	tttgcnaaat	ttccaaaact	720
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cnttnttaa	attgaacctn	aattcncccc	cccaaaaaaaaaa	aaccncnong	ggggcggtat	900
ttccaaaaac	naattccctt	accaaaaaaaaac	aaaaaaccnc	ccttnttccc	ttccnccctn	960
ttcttttaat	tagggagaga	ttaagcccc	caatttccng	gnctngatnn	gtttcccccc	1020
ccccccattt	ccnaaacttt	ttcccancna	ggaancncc	cttttttng	gtcngattna	1080
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atagan						1146

<210> 10
 <211> 545
 <212> DNA
 <213> Homo sapien

<400> 10

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tattggctct	gagttcttag	gccagtttc	ttcttctgtt	gagtagtgcgg	gattgtcagg	180
cagatctggc	tgtggaaagg	agactgtggg	cagcaagttt	agaggcgtga	ctgaaagtca	240
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cttttgcgt	ccttacagt	ggattacagc	cacctgctga	ggtgagtagc	ccacgctcct	360
ggttagatggc	tccacgtaca	tgcacagttag	caaaggcgta	cctgctgtca	gtgttaacgt	420
taatatcctt	accccatcg	agagcctgag	tgagggcgat	caattcagcc	cttttgtgct	480
gaggtgtttt	ctgggttaagc	cctgaaccca	caacacatct	gtctccatgg	taacagctgc	540
accgg						545

<210> 11
 <211> 196
 <212> DNA
 <213> Homo sapien

<400> 11

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ggggggatcg	cttgcaccca	agatttcaag	actagtctgg	gtaacatagt	gagaccctat	120
ctctacgaaa	aaataaaaaaa	atgagcctgg	tgtatggca	cacaccagct	gaggagggag	180
aatcgagcct	aggaga					196

<210> 12
 <211> 388
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(388)
 <223> n = A,T,C or G

<400> 12

tctccttaggc ttgggggctc tgactagaaa ttcaaggaac ctgggattca agtccaactg	60
tgacaccaac ttacactgtg gnctccaata aactgcttct ttcctattcc ctctctatta	120
aataaaaataa ggaaaacgat gtctgtgtat agccaagtca gntatcctaa aaggagatac	180
taagtgacat taaatatcag aatgtaaaac ctgggaacca ggttcccagc ctgggattaa	240
actgacagca agaagactga acagtaactac tgtaaaaagc ccgaagnngc aatatgttca	300
ctctaccgtt gaaggatggc tgggagaatg aatgctctgt cccccagtc caagctcact	360
tactatacct cctttatagc ctaggaga	388

<210> 13

<211> 337

<212> DNA

<213> Homo sapien

<400> 13

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taccctgaaa aatatgaggg aatatatga aacagggagg caatgtttag ataattgtac	120
acaagatatg atttctacat cagatgctct ttcctttcct gtttatttcc ttttatttc	180
ggttgtgggg tcgaatgtaa tagctttgtt tcaagagaga gttttggcag tttctgttagc	240
ttctgacact gctcatgtct ccaggcatct atttgcactt taggaggtgt cgtggagac	300
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<210> 14

<211> 571

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(571)

<223> n = A,T,C or G

<400> 14

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agtgttcaggc tgggttttt tactgtaaac aataaggaga ctttgctctt cattaaacc	120
aaaatcatat ttcatatttt acgctcgagg gtttttaccg gttcctttt acactccta	180
aaacagttt taagtcgttt ggaacaagat atttttctt tcctggcagc ttttaacatt	240
atagcaaatt tggctctggg ggactgctgg tcactgtttc tcacagtgc aaatcaaggc	300
atttgcacc aaaaaaaaaa atttttttt ttttatttga aactggaccc gataaacgg	360
gtttggagcg gctgctgtat atagttttaa atggttattt gcacccctt aagttgcact	420
tatgtggggg ggggnntttg natagaaagt nttaatcacc anagtcacag ggactttnt	480
cttttggnnna ctgagctaaa aaggcgtgmt tttcgggtgg gggcagatga aggctcacag	540
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<210> 15

<211> 548

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(548)

<223> n = A,T,C or G

<400> 15

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taaaaagtatt tccaaaaggc ataaaaccaa agtatcatac caaaccaaatt tcataactgct	120
tccccccaccc gcactgaaac ttcaccttct aactgtctac ctaaccaaatt tctacccttc	180
aagtctttgg tgcgtctca ctactcttt tttttttttt ttnntttgg agatggagtc	240
tggctgtgca gcccagggtt ggagtacaat ggcacaacct cagctactg naacctccgc	300
ctcccaggtt catgagattc ttctgnttca gccttccag tagctggac tacaggtgt	360
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ggccaggngt gtnctgaact cctgacctca agtgatccac ccacctaagg ctccaaagt	480
gtctaggatta cagacatgag ccactgngcc cagnctggc gcatgctcac ttctcttaggc	540
aactacta	548

<210> 16

<211> 638

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(638)

<223> n = A,T,C or G

<400> 16

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gcaatccgag cctatccctca agatgagttt ttagaaagaa ttgatattgc gatagaccaa	120
gctggtaagc actctgacta cacgaaattt ttcatgtg atggattttt gacagtttat	180
ctttggaaaga gattattaag tgattattttt aaaggaaatc cattaattcc agaatatctt	240
ggtttagctc aagatgatata agaaatagaa cagaaagaga ctacaaatga agatgtatca	300
ccaaactgata ttgaagagcc tatagtagaa aatgaatttgcattttt tagccttaca	360
catagcgatt ttccctgatga atcttatattt cagccatcga catagcatta cctgatggc	420
aaccttacga ataataaaaaa ctgggtgcgg ggctattgtt gaattcatcc ncagtaaatt	480
tggatatnac aaaatataac tcgatttgcattt ttggatgtt gaataactaaa tctggcaaaa	540
gtaactttgg agctactagt aacctcttctt ttggatgttcaaaaattttctt ttttagggttt	600
cttattctctt acttacgga tattggagca taacggga	638

<210> 17

<211> 286

<212> DNA

<213> Homo sapien

<400> 17

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gtgcgcggcg attggctgt ttatctcaaa caccgcacg gcggtgtga tggcgccat	120
tgccttagcg gcccggaaatg caatggcgat ctcaccctat cttttgcac ttgtgggtgc	180

gatggcggct tcggccgcgt ttatgacccc ggtctcctcg ccggtaaca ccctggcgct	240
tggccctggc aagtactcat ttagcgatt tgtcaaaaata ggcgtg	286
<210> 18	
<211> 262	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(262)	
<223> n = A,T,C or G	
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tagccttaca ttttatagc ctcctccctg gtctgtctt tgattttctt gcctgtaatc	120
catatcacac ataactgcaa gtaaacattt ctaaaagtgtg gttatgctca tgtcaactcct	180
gtgncaagaa atagttcca ttaccgtctt aataaaaattt ggatttgttc tttnctattn	240
tcactcttca cctatgaccg aa	262
<210> 19	
<211> 261	
<212> DNA	
<213> Homo sapien	
<400> 19	
tcggtcata caaagccagt ggttttagct ctctactgtg taaaactccta aaccaggcc	60
atttatgata aatggggca ggattttat tataaacatg tacccatgca aatttcctat	120
aactctgaga tatattctt tacattnaa caataaaaat aatcttattt taaaagccta	180
atttgcgtat ttaggtttaga gtgtttatg agagggtata aggtataat caccagtcaa	240
cgtttctctg cctatgaccg a	261
<210> 20	
<211> 294	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(294)	
<223> n = A,T,C or G	
<400> 20	
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cgataggcgc cggccagcca gcgaaacgggt tgcccgatg gcgaaggcag ccggagttct	120
tcggactgag tatgaatctt gttgtgaaaa tactcgccgc cttcgatcgca cgacgtcgcg	180
tcgaaatctt cgancctt acgatcgaaat tcttcgtggg cgacgatcgca ggtcaagtcc	240
gccccaccga aatcatggtt gagccggatg ctgncccgaa agncctcgat tgn	294
<210> 21	
<211> 208	

<212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(208)
 <223> n = A,T,C or G

<400> 21
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 atcaatgaat aggaaaattc ccaaagaggg aatgtcctgt tgctcgccag ttttntgtt 120
 gttctcatgg anaaggcaan gagctctca gactattggn attntcggtc ggtcttctgc 180
 caactagtcg ncttgcnang atcttcat 208

<210> 22
 <211> 287
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(287)
 <223> n = A,T,C or G

<400> 22
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 gtggcgggtc acccggcagt gggctcccg acaggccagc aggatttggg gcaggtacgg 120
 ngtgcgcac ngtgcgcac ngtgcgcac ngtgcgcac ngtgcgcac ngtgcgcac 180
 ggcgctggag ctttccacgg tccatgnatt gngatggctg ttctaggcgg ctgttgccaa 240
 gcgtgatggt acgctggctg gagcattgat ttctggtgcc aaggtgg 287

<210> 23
 <211> 204
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(204)
 <223> n = A,T,C or G

<400> 23
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 gggccaagct gtggccgggg atggtgaga actgaagcgg gacctcctcg aggtcctccg 120
 ncgttacttc nccgtccagg aggagggtct ttccgtggtc tnggaggagc gggggggagaa 180
 gatnctcctc atggtnaca tccc 204

<210> 24
 <211> 264
 <212> DNA
 <213> Homo sapien

<220>		
<221> misc_feature		
<222> (1) ... (264)		
<223> n = A, T, C or G		
<400> 24		
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gtcctaaatg atagttgctg agtttttctt tgaccatga gttatattgg agtttat	120	
ttaactttcc aatcgcatgg acatgttaga cttat	180	
ttaaattgga tttgagaaaat tggtnnttata tataatcaatt tttggattttt gttgagttt	240	
acattatagc ttagtatgtg acca	264	
<210> 25		
<211> 376		
<212> DNA		
<213> Homo sapien		
<220>		
<221> misc_feature		
<222> (1) ... (376)		
<223> n = A, T, C or G		
<400> 25		
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gtcaagggtt catgagtcat gatttgcca ctgcactcca gcctgggtga cagaccgaga	180	
ccctgcctca anaganaang aataggaagt tcagaaatcn tggntgtgn gcccagcaat	240	
ctgcatctat ncaaccctg caggcaangc tgatgcagcc tangttcaag agctgctgtt	300	
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gtcctccgtt tgnac	376	
<210> 26		
<211> 372		
<212> DNA		
<213> Homo sapien		
<220>		
<221> misc_feature		
<222> (1) ... (372)		
<223> n = A, T, C or G		
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gttcaagggtt gcatgagtca tgatcgcc actgcactcc agcctgggtg acagactgag	180	
accctgcctc aaaagaaaaa gaataggaag ttcagaaacc ctgggtgtgg ngcccagca	240	
tctgcattta aacaatccct gcaggcaatg ctgatgcagc ctaagttcaa gagctgctgt	300	
tctggaggca gnagtaaggg cttccatcca gcatcacggc caacactgca aaagcacctg	360	
tcctcggtt ta	372	

<210> 27	
<211> 477	
<212> DNA	
<213> Homo sapien	
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cctacattga aaagagaagt tgctaaaagg tgcacaggaa atcattttt taagtgaata	120
tgataatatg ggtccgtgct taatacaact gagacatatt tgttctctgt ttttttagag	180
tcacctctta aagtccaatc ccacaatggt gaaaaaaaaa tagaaagtat ttgttctacc	240
tttaaggaga ctgcaggat tctccttcaa aacggagtat ggaatcaatc ttaaataaaat	300
atgaaattgg ttggcttct gggataagaa attcccaact cagtgtgctg aaattcacct	360
gactttttt gggaaaaaat agtcgaaaat gtcaatttg tccataaaaat acatgttact	420
attaaaagat atttaaagac aaattcttc agagctctaa gattggtgac gacagaa	477
<210> 28	
<211> 438	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (438)	
<223> n = A,T,C or G	
<400> 28	
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attccagcaa aatccctcta gttttggag tttccttta cttatctgggg ctgcctgagc	120
cacaaatgcc aaattaagag catggctatt ttcgggggct gacaggtcaa aagggtgtaa	180
aatccgataa gcctcctgga ggtgctctaa aaacactcct ggtgactcat catgcccctg	240
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attaggtccc aattgggtct ctaatcacta ttccctctagc ttccctccctc ggnctattgg	420
ttgatgtgag gttgaaga	438
<210> 29	
<211> 620	
<212> DNA	
<213> Homo sapien	
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<221> misc_feature	
<222> (1) ... (620)	
<223> n = A,T,C or G	
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agaagtcaaa aattgagttt tgggatccctc agccttagatt tcagaggata taaagaaaca	120
cctaaccct agatattcag acaaaagttt actacaggga tgaagcttc acggaaaacc	180
tctacttaga aagtacagaa gagaaatgtg gtttggagc ccccaaacag aatccctct	240
agaacactgc ctaatgaaac tgtgagaaga tggccactgt catccagaca ccagaatgat	300

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ccatgaaaaa aaaactgaga agaagactgt nccctacaat gccaccggag cagaactgcc	420
ccaggccatg gaagcacagc tcttatatca atgtgacctg gatgttgaga catggaatcc	480
nangaaatcn tttaaanact tccacggtn aatgactgcc ctattanatt cngaacttan	540
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cccatgcctg tncccttta	620
<210> 30	
<211> 100	
<212> DNA	
<213> Homo sapien	
<400> 30	
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<210> 31	
<211> 762	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(762)	
<223> n = A, T, C or G	
<400> 31	
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acactcttcc tgaaaagaga aagaaaagag gcaggaaaga ggttaggatt tcattttcaa	120
gagtcagcta attaggagag cagagtttag acagcagtag gcaccccatg atacaaacca	180
tggacaaagt ccctgtttag taactgccag acatgatcct gctcagggtt tgaatctct	240
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cnctgaagga attcttaaaa ccctttgtga gaaatgccc ccttaccatg acaantggtc	720
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<211> 276	
<212> DNA	
<213> Homo sapien	
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cacaaccagt aaattggcag agtcagattt gaatccatgg agtctggct gcactttcaa	180
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<210> 34						
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<212> DNA						
<213> Homo sapien						
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ggcgcattt	ctgggaaagg	ctcagatcca	cctactgctc	cttgctcg	tattgtttt	540
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actgatacca	tgaaacctac	ttggagcaga	cattgcacag	ttttctgtgg	taaaaaactaa	180
aggttttattt	gtctagctgt	catcttatgc	tttagtatttt	ttttttacag	tggggatttg	240
ctgagattac	attttgttat	tcattagata	ctttgggata	acttgacact	gtcttctttt	300
tttcgctttt	aattgctatc	atcatgctt	tgaacaacaaga	acacattagt	cctcaagtat	360
tacataagct	tgcttggta	gcctgggtgt	ttaaaggact	atctttggcc	tcaggttcac	420
aagaatgggc	aaagtgttcc	cttatgttct	gtagttctca	ataaaagatt	gccaggggcc	480
gggtactgtg	gctcgactg	taatcccagc	acttgggaa	gctgaggctg	gcggatcatg	540
ttagggcagg	tgttcgaaac	cagcctggc	aactacta			578

<210> 36
 <211> 583
 <212> DNA
 <213> Homo sapien

<400> 36

tagtagttgc ctgtatccc agcaacttag gaggctgggg caggagaatc agttgaacct	60
gggaggcaga agttgtattt agcaaagatc gcaccattgc acttcagcct gggcaacaag	120
agttagattc catctcaaaa acaaaaaaaa gaaaaagaaa agaaaaggaa aaaacgtata	180
aacccagcca aaacaaaatg atcattctt taataagcaa gactaattt atgtgtttat	240
ttaatcaaag cagttgaatc ttctgagttt ttggtaaaaa tacccatgtt gtttatttag	300
gttcttact tgggtgaacg tttgatgtt acagttata aaatggttaa caaggaaaat	360
gtatgcataaa gaatcttata aactactaaa aataaataaa atataaatgg ataggtgcta	420
tggatggagt ttttgtttaa tttaaaaatct tgaagtcatt ttggatgctc attgggttgc	480
tggtaatttc cattaggaaa aggttatgtt atggggaaac tttttcttga aattgcggaa	540
tgtttctcat ctgtaaaatg ctgtatctc agggcaacta cta	583

<210> 37
 <211> 716
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(716)
 <223> n = A,T,C or G

<400> 37

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gtttttttgt tctttatcc agacccttat atatgtttat gttcacaggc agggcaatgt	120
ttagtggaaa caattctaaa ttttttattt tgcatttca tgctaatcc cgtcacactc	180
cagcaggctt cctggggagaa taaggagaaa tacagctaaa gacattgtcc ctgttactt	240
acagcctaat ggtatgctaaa accacttcaa taaagtaaca ggaaaagttac taaccaggta	300
gaatggacca aaactgatata agaaaaatca gaggaagaga ggaacaaata tttactgagt	360
cctagaatgt acaaggcttt ttaattacat attttatgtt aggcctgcaa aaaacaggtg	420
agtaatcaac atttgtccca ttttacatat aagggaaactg aagcttaat tgaataattt	480
aatgcataaga ttttataatgtt agaccatgtt caggtcccta tttttataactt actagctgtt	540
tgaatatgag aaaataattt tgtttatttc ttggcatcag tttttcatc tgcaaaataa	600
agctaaaggat atttagctaaa cagtcagcat agtgcctgtt acatagtagg tgctccaaac	660
atgattacnc tantatnngg tattanaaaa atccaatata ggcntggata aaaccg	716

<210> 38
 <211> 688
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(688)
 <223> n = A,T,C or G

<400> 38	
ttctgtccac atatcatccc actttaattt ttaatcagca aaactttcaa tgaaaaatca	60
tccatttaa ccaggatcac accagggaaac tgaaggtgta ttttttttta ccttaaaaaaa	120
aaaaaaaaaaa accaaacaaa ccaaaacaga ttaacagcaa agagttctaa aaaatttaca	180
tttctcttac aactgtcatt cagagaacaa tagttctaa gtctgttaaa tcttggcatt	240
aacagagaaa cttgatgaan agttgtactt ggaatattgt ggattttttt ttttgtctaa	300
tctccccccta ttgttttgc aacagtaatt taagttgtg tggaacatcc ccgtagttga	360
agtgtaaaca atgtatagga aggaatataat gataagatga tgcatcacat atgcattaca	420
tgtagggacc ttcacaactt catgcactca gaaaacatgc ttgaagagga ggagaggacg	480
gcccagggtc accatccagg tgccttgagg acagagaatg cagaagtggc actgttggaa	540
tttagaagac catgtgtgaa tggtttcagg cctggatgt ttgccaccaa gaagtgcctc	600
cgagaaattt ctttcccatt tggaaatacag ggtggcttga tgggtacggt gggtgaccca	660
acgaagaaaa tggaaattctg ccctttcc	688
<210> 39	
<211> 585	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(585)	
<223> n = A,T,C or G	
<400> 39	
tagtagttgc cgcnaccta aaantggaa agcatgtatgt ctaggaaaca tantaaaata	60
gggtatgcct atgtgctaca gagagatgtt agcattaaa gtgcattttt ttatgttattt	120
tgacaaatgc atatnccctc ataatccaca actgattacg aagctattac aattaaaaag	180
tttggccggg cgtggctggc ggtggctgac gcctgtaatc ccagcacattt gggaggccga	240
ggcacgcgga tcacgaggc gggagttcaa gaccatcctg gctaacacgg tgaagtccttca	300
tctctactaa aaatacgaaa aaattacccc ggcgtggtgg cgggcgcctg tagtcccagc	360
tactccggag gctgaggcag gagaatggcg tgaacccagg acacggagct tgcagtgtgc	420
caacatcactg tcactgcctt ccagcctggg ggacaggaac aagantcccg tcctcanaaa	480
agaaaaataac tactnatant ttcnacttta ttttaantta cacagaactn cctttggta	540
cccccttacc attcatctca cccacctcctt atagggcacn nctaa	585
<210> 40	
<211> 475	
<212> DNA	
<213> Homo sapien	
<400> 40	
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taacatgtat ttatggacc aaattgacat ttgcactgt tttttccaaa aaagtcaagg	120
gaatttcagc acactgagggtt gggaaatttctt tatccagaa gaccaaccaa tttcatattt	180
atttaaaggatt gattccatac tccgttttca aggagaatcc ctgcagtctc cttaaaggta	240
gaacaaatac ttccattttt ttttccacca ttgtgggatt ggactttaa aggtgactct	300
aaaaaaaaacag agaacaaata tgcgtcagggtt gtatataagca cggacccata ttatcatatt	360
cactaaaaaa aatgatttcc tgcgtcagggtt ttggcaactt ctctttcaa tgcgtggaaa	420
aacttagtca ccctgaaaac ccacaaaata aataaaactt gtagatgtgg acaga	475

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<210> 41
<211> 423
<212> DNA
<213> Homo sapien

<400> 41
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aaaaaaaaatc taagtattta taagggtata ggtaacattt aaaagttaggg ctagctgaca
ttattnagaa agaacacata cgagagata agggcaaagg actaagacca gaggaacact
aatatttagt gatcacttcc attcttggta aaaatagtaa ctttaagtt agcttcaagg
aagattttg gcacatgatta gttgtcaaaa gttagttctc ttgggtttat attactaatt
ttgttttaag atccttgtta gtgcatttaat aaagtcatgt tatatcaaac gctctaaaac
attgttagcat gttaaatgtc acaataact taccatttgc tttatatggc tttaccctct
cta

<210> 42
<211> 527
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(527)
<223> n = A,T,C or G

<400> 42
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aaaaagctta tagaataaga atatgaagaa agaaaatattttt tacatttgcacaaatga
gtttatgttt taagctaagt gttattacaa aagagccaaa aagttttaa aaattaaaac
gtttgttaag ttacagtacc cttatgttaa ttataattt aagaaagaaaa aactttttt
tataaatgtt gtgttagccta agcatacagt atttataaag tctggcagtg ttcaataatg
tccttaggcct tcacattcac tcactgactc acccagagca acttccagtc ctgttaagctc
cattcgttgtt aagtgcctta tacaggtgca ccatttattt tacagtattt ttactgtacc
ttctctatgt ttccatatgtt tcgatatac aaataccact ggttactatn gcccnaacagg
taattccagt aacacggcct gtatacgtct gttttttttt gngaaaga

<210> 43
<211> 331
<212> DNA
<213> Homo sapien

<400> 43
tcttcaacccctt cgttaggacaa ctctcatatg cctgggcact attttaggt tactacccctt
gctgccttc tttaagaaaa aaaaaagaag aaaaaagaac ttttccacaa gtttcttttc
ctcttagttgg aaaaatttagag aaatcatgtt ttatattttt gtttatttca gatcacaat
tcaaacactt gtaaacatcca agcttctgtt caatccccctt ggaagaggat tcattctgtat
atttacggtt caaaaagaagt tgtaatattt gttttggaaac acagagaacc agtttataac
ttcttactac tattatataa taaataataa c

<210> 44

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<211> 592
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(592)
 <223> n = A,T,C or G

<400> 44

ggcttagtag ttgccaggca aaatarcgtt gatttcctc aggagccacc cccaacaccc	60
ctgtttgctt ctagacctat acctagacta aagtcccagc agacccttag aggtgagggtt	120
cagagtgacc cttgaggaga tgtgctacac tagaaaagaa ctgcttgagt tttctaattt	180
atataagcag aaatctggag aagagtctata ggaatggata ttaagggtgt gagataatgg	240
cggaaaggaat atagagttgg atcaggctgg acttattgtat ttgaacccac taagtagaga	300
ttctgctttt gatgttgcag ctcagggagt taaaaaaggt ttaatggtt ctaatagttt	360
atttgctgg ttagctgaaa tatggataaa agatggccca ctgtgagcaa gctggaaatgg	420
cctgtatctct ctcagttaa tgtagaggaa gggatccaaa agtttaggga ganttggatg	480
ctggraktgg attggtaact ttgrgaccta cccwtcccag ctgggagggt ccagaagata	540
cacccttgcac caacgctttt cgaaatggat ttgtgatggc ggcaactact aa	592

<210> 45
 <211> 567
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(567)
 <223> n = A,T,C or G

<400> 45

ggcttagtag ttgccattgc gagtgcttgc tcaacgagcg ttgaacatgg cggattgtct	60
agattcaacg gatttgagtt ttaccagcaa agcgaaccaa ggcggccca gagaattatgg	120
ggttgggtgg ctttggaaatgg atggaaatcc tgttaggcata gtcagaaaaag ctttcttgc	180
gaacagttgg ttctcggcg aacgctcatc aagatgcccata ttggaaaggc tagcgtgtat	240
ttgggagagc ctgatagcgt gtcttctgtat gatgtttgtt cttggacagt gacaaaagat	300
atgcaaaagca agtccgaact agacgtcaag cttcggtgaaatatttgc agactcctac	360
ttatactgtg aggaatgata gccaagggtt gggactttaa gactaagggtt gtttgcactt	420
gcccggatgatc tcccgaggcag aaagamctga tcgctagttt tatacgggca actactaagc	480
cgaattccag cacactggcg gccgttacta attggatccg anctcggtac cagcttgc	540
catascttga gttwtctata ntgtcnc	567

<210> 46
 <211> 908
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(908)

<223> n = A,T,C or G

<400> 46

gagcgaaaga ccgagggcag ngnntangng	cgangaagcg gagagggcca	aaaagcaacc	60
gctttccccg gggggtgccg attcattaag	gcaggtggag gacaggttc	ccgatggaag	120
gccccgcagggg cgcaagcaat taatgtgagt	aggccattca ttagcacccg	ggctaacat	180
ttaagcttcg ggttgttatg tgggtggaat	tgtgagcga taacaatttc	acacaggaaa	240
cagctatgac catgattacg ccaagctatt	taggtgacat tatagaataa	ctcaagttat	300
gcatcaagct tggtaccgag ttcggatcca	ctagtaacgg ccgcccagtgt	gtggaattcg	360
gcttagtagt tgccgaccat ggagtgtac	ctaggctaga atacctgagy	tcctccctag	420
cctcaactcac attaaattgt atctttcta	cattagatgt cctcagcgcc	ttatttctgc	480
tggacwatcg ataaattaaat cctgataga	tgatagcgc agattaatta	ctgagagat	540
gttaatgtgt catccctcct atataacgta	tttgcatttt aatggagcaa	ttctggagat	600
aatccctgaa ggcaaaggaa tgaatcttga	gggtgagaaaa gccagaatca	gtgtccagct	660
gcagttgtgg gagaaggtga tattatgtat	gtctcagaag tgacaccata	tgggcaacta	720
ctaagcccgaa attccagcac actggcgggc	gttactaatg gatccgagct	cggtaccaag	780
cttcatgtcat agctttagtgc tctatagtgt	cactaaatag cctggcgta	tcatggtcat	840
agctgtttcc tgtgtgaaat tgttatccgc	tcccaattcc ccccaccata	cgagccggaa	900
cataaaagt			908

<210> 47

<211> 480

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (480)

<223> n = A,T,C or G

<400> 47

tgccaacaag gaaagttta aatttccct tgaggattct	tggtgatcat caaattcagt	60
gttttttaag gttgtttct gtcaaataac tctaacttta	agccaaacag tatatggaag	120
cacagataka atattacaca gataaaagag gagttgatct	aaagtaraga tagttgggg	180
ctttaatttc tggAACCTAG gtctcccat cttctctgt	gctgaggaac ttcttggag	240
cggggattct aaagttctt ggaagacagt ttgaaaacca	ccatgttgc ttcgtacct	300
ttatTTTaa aaagttaggtg aacatTTGA gagagaaaag	ggcttgggg agatgaagtc	360
cccccccccc cttttttttt ttttagctga aatagatacc	ctatgttnaa rgaarggatt	420
attatTTacc atGCCAYtar scacatgctc tttgatggc	nyctccstac ctccttaag	480

<210> 48

<211> 591

<212> DNA

<213> Homo sapien

<400> 48

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tggccaaacat tacgaacttc caactcaacc	gttcttggac gttcaagcgg	gagtaccggc	120
gaggatggtg gcgtgaattc tggccttct	ttgcgtggg atcggtagcc	gccatcatcg	180
gtatgtttat caagatcttc ttactaacc	cgacctctcc gatttacctg	cccgagccgt	240
ggTTAACGA ggggaggggg atccagtac	gctgactg	gtcccagatc	300

<211> 392	
<212> DNA	
<213> Homo sapien	
<400> 52	
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gcaataatta tctgagaaaa aaaagtgggtg aaagattaaa cttgcatttc tctcagaatc	120
tttgaaggata tttgaataat tcaaaaagcg aatcagtagt atcagccgaa gaaactca	180
tagctagaac gttggaccctc tggatctaag tccctgcctc tccactaacc agctgattgg	240
ttttgtgtaa acctcctaca cgcttgggtc tggtcgcctc atttgtcaaa gtaaaggctg	300
aaataggaag ataatgaacc gtgtctttt ggtctctttt ccatccattt ctctgatttt	360
acaaagaggc ctgtattccc ctggtgaggt tg	392
<210> 53	
<211> 179	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(179)	
<223> n = A,T,C or G	
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tttcagattc ctgtaaacctt ctaaagaaaa ggagtgcgc ctcactgtat gtagaaatga	120
ctagttcagc atacngagac acntctgact ccgattctag aggactgagt gacctgcan	179
<210> 54	
<211> 112	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(112)	
<223> n = A,T,C or G	
<400> 54	
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tgcattttcc cacanacaaa attcaaatga ntggaagaaaa ttggganagt at	112
<210> 55	
<211> 225	
<212> DNA	
<213> Homo sapien	
<400> 55	
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aaaggagtagt atccaaatgc caataaacat ataaaaagga attcagctc atcatcatca	120
gaagwatgca aattaaaacc ataatgagaa accactatgt cccactagaa tagataaaat	180

cttaaaaagac tggtaaaacc aagtgttggt aaggcaagag gagca	225
<210> 56	
<211> 175	
<212> DNA	
<213> Homo sapien	
<400> 56	
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tttagtattgg gatttaccc ctgtcctata aagatgttat gtacaaaaaa tgaagtggag	120
ggccatataccc tgagggaggg gagggatctc tagtgttgc agaagcggaa gctca	175
<210> 57	
<211> 223	
<212> DNA	
<213> Homo sapien	
<400> 57	
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ttgttaattt tggtttttt ctgtgaaaca catacattgg atatggagg taaaggagtg	120
tcccagttgc tcctggtcac tcccttata gccattactg tcttgttct tgtaactcag	180
gttaggtttt ggtctctctt gctccactgc aaaaaaaaaaaa aaa	223
<210> 58	
<211> 211	
<212> DNA	
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<210> 59	
<211> 208	
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aggctgcaca tcaggggact gcctcgcaat acttcatgct gttgctgctg actgatggtg	180
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cagtatcat tatgggtggt aaatggct	
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<211> 171	
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<213> Homo sapien	
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aaccactgac accagttggc aatagcttct tccttcttta acctctttaga gtatttatgg	120
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<210> 61	
<211> 134	
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<221> misc_feature	
<222> (1)...(134)	
<223> n = A,T,C or G	
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canaatcatc nggc	134
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<211> 145	
<212> DNA	
<213> Homo sapien	
<400> 62	
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gccattnaat caataagtga tagagtcaag gctcaaccca ggtgtgacgg attccaggc	120
ccaagctcct tactggtacc cttt	145
<210> 63	
<211> 297	
<212> DNA	
<213> Homo sapien	
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ccacagtcag cgccatggtg gtccggtaaa gcatttggtc aggcaggcct cgttcaggt	180
agacgggcac acatcagctt tctggaaaaa ctttgtgc tctggagctt tgttttccc	240
agcataatca tacactgtgg aatcgaggat cagtttagtt ggttaaggca gaggagc	297
<210> 64	
<211> 300	
<212> DNA	
<213> Homo sapien	
<400> 64	
gcactgagag gaacttccaa tactatgtt aataggagtg gtgagagagg gcatccttgt	60
cttgtgccgg tttcaaaagg gaatgcttcc agctttgcc cattcagtagt aatattaaag	120
aatgttttac cattttctgt cttgcctgtt tttctgtttt tttgttggc tcttcattct	180
ccattttag gccttacat gtttaggaata tattttttt aatgataactt caccttgggt	240

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tcgatagaag ttcctctcag tgc	203
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<212> DNA	
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tgcagtctg gtagcaggag ttctgtgctt tggggctaa ggctcctgga tgacccctga	120
catggagaag gcagagttgt gtgccttc tcatggcctc gtcaaggcat catgactgc	180
cacacacaaa atgcccttt tattaacgac atgaaattga aggagagaac acaattca	240
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<210> 67	
<211> 157	
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taaccagact gatagccatt ggatggataa tatggtggtt gaggaggac actactata	120
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tgaggaggca tcacccg	137
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<213> Homo sapien	

<400> 69	
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gaagttcctc tcagtgc	137
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aaargaagac atytattcag ccagtaaaca yataaaaaaa aggctcatsa tcactgawca	240
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tcaaagttcc catgctgcca aagtgccatc ctttgggta ctgtttctg agctccagtg	180
ataactcatt tatacaaggg agataccag aaaaaaagtg agcaaatctt aaaaaggtgg	240
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<220>
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<210> 136
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<210> 139
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<210> 140
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<210> 141
 <211> 9388
 <212> DNA
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<400> 141

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<211> 419

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<213> Homo sapien

<400> 142

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<211> 402

<212> DNA

<213> Homo sapien

<400> 143

<210> 144

<211> 224

<212> DNA

<213> Homo sapien

<400> 144

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<211> 111

<212> DNA

<213> Homo sapien

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<211> 585

<212> DNA

<213> Homo sapien

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 <212> DNA
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<210> 154
 <211> 345
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (345)
 <223> n = A,T,C or G

<400> 154

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tcaagattcc ataggctgac ctggacagag atctcctggg tctggccag gacagcaggc      60
tcaagcttag tggagaagg ttcctatgacc ctcatgatcc cccaaacctt ggattgggtg      120
acattgcattt tccttagaga gggaggagat gtangtctgg gcttccacag ggacctggta      180
tttttaggatc agggtaccgc tggcctgagg cttggatcat tcanagcctg ggggtgaaat      240
ggctggcagc ctgtggccccc attgaaatag gctctggggc actccctctg ttccctanttg      300
aacttggta aggaacagga atgtggcan cctatggaat cttga      345
  
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<210> 155
 <211> 295
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1) ... (295)
 <223> n = A,T,C or G

<400> 155

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gacgcttggc cacttgacac attaaacagt tttgcataat cactancatg tatttctagt      60
ttgctgtctg ctgtgatgcc ctgcctgtat tctctggcgt taatgatggc aagcataatc      120
aaacgctgtt ctgttaattc caagttataa ctggcattga ttaaaggcatt atcttcaca      180
actaaaactgt tcttcatana acagcccata ttattatcaa attaagagac aatgtattcc      240
aatatcctt anggccaata tatttnatgt cccttaatta agagctactg tccgt      295
  
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<210> 156
 <211> 406
 <212> DNA

```

<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(406)
<223> n = A,T,C or G

<400> 156
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aggtgtggctt ggggtgagtg ggtggggaa gtgtgtgtc aaaggggggtg tnaatgtnta
tgcgtgtgag catgagtgtat ggctagtgatc actgcattgtc agggagtggtg aacaagcgtg
cgggggtgtg tggcaagtgt cgtatgcata tgagaatatgt tgcgtgtggta tgagtgcatt
tggaaagtctg tgcgtgtgcgt tgcgtgtcatg anggttaantt antgactgcgt caggatgtgt
gagtgtgtcat ggaacactca ntgtgtgtgt caagtggccn ancgtc 60
120
180
240
300
360
406

<210> 157
<211> 208
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(208)
<223> n = A,T,C or G

<400> 157
tgacgcttgg ccacttgaca cactaaagggtgttactcat cactttcttc ttcctcggt
ggcatgtgag tgcatttattt cacttggcac tcattttttt ggcagtgtact gtaanccana
tctgtatgtcat acaccagctt gtaaaattgaa taaatgtctc taataactatgt tgctcacaat
anggtanggg tgaggagaag gggagaga 60
120
180
208

<210> 158
<211> 547
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(547)
<223> n = A,T,C or G

<400> 158
cttcaacctc cttcaacctc cttcaacctc ctggattcaa acaatcatcc cacctcagac
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agggtttcat catgttgcctc tggctggctt caaaactcctg acctcaagca atgtgcccac
ctcagcctcc caaagtgtctt ggattacagg cataagccac catgcccagt ccatntttaa
tctttcttac cacattctta ccacacttcc ttttatgtttt agatacataa atgcttacca
ttatgatatacatttgcaca gtatggac agtaacatgc tgcacaggtt tgcgtgttag
gaacagtagg caataccaca tagcttaggt gtgtggtaga ctataccatc taggtttgtg
taaqtacac ttatqctqt ttacacaatq acaaaccat ctaatgtgc atttctcaga 60
120
180
240
300
360
420
480

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atgtatcctt gtcagtaagc tatgatgtac aggaaacact gcccaaggac acagatattg	540
tacctgt	547
<210> 159	
<211> 203	
<212> DNA	
<213> Homo sapien	
<400> 159	
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aacagcctgt atccaaacac ttaacacact cacctgaaaa gttcaggcaa caatgcctt	120
ctcatgggtc tctctgtcc agttctgaac ctttctcttt tcctagaaca tgcatttarg	180
tcgatagaag ttctctcag tgc	203
<210> 160	
<211> 402	
<212> DNA	
<213> Homo sapien	
<400> 160	
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taaacaataa taataatatt tagcatttat agagcacttt atatcttcaa agtacttgca	120
aacattayct aattaaatac cctctctgtat tataatctgg atacaaatgc acttaaaactc	180
aggacagggt catgagaraa gtagcattt gaaagttggt gctagctatg ctttaaaaac	240
ctataacaatg atgggraagt tagagttcag attctgttgg actgtttttg tgcatttcag	300
ttcagcctga tggcagaatt agatcatatc tgcactcgat gactytgctt gataacttat	360
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<210> 161	
<211> 193	
<212> DNA	
<213> Homo sapien	
<400> 161	
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actgaccagg agaaaaacca accaataaaa acaggcccgg acataagaca aataataaaa	120
ttagcggaca aggacatgaa aacagctatt gtaagagcgg atatagtggt gtgtgtctgg	180
gctcaacatg cta	193
<210> 162	
<211> 147	
<212> DNA	
<213> Homo sapien	
<400> 162	
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gacaataat aaaattagcg gacaaggaca tgaaaacagc tattgtaaga gcggatata	120
tggtgtgtgt ctgggctcaa catgcta	147
<210> 163	
<211> 294	

<212> DNA
 <213> Homo sapien

<400> 163

tagcatgttg agccagaca caaatcttc cttaagcaat aaatcatttc tgcatatgtt	60
tttaaaccca cagctaagcc atgattattc aaaaggacta ttgtattggg tattttgatt	120
tgggttctta tctccctcac attatcttca tttctatcat tgacctctta tcccagagac	180
tctcaaactt ttatgttata caaatcacat tctgtctcaa aaaatatctc acccacttct	240
cttctgttgc tgctgtgtta tgtgtgtgtg tgtgtgtctg ggctcaacat gcta	294

<210> 164
 <211> 412
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(412)
 <223> n = A,T,C or G

<400> 164

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cacctggctg caagtgcgcc agagccgccc tgactacgtg ctgctgtgg gctggggcgt	120
gatgaactcc accgcctga aggaagccca ggccaccgga taccggcccg acaagatgt	180
cggcgtgtgg tggcccggtg cggagcccgta tggcgtgac gtggcgaag gcgccaagg	240
ctacaacgcg ctggctctga acggctacgg cacgcagtcc aaggtgatcc angacatcct	300
gaaacacgtg cacgacaagg gcaaggcac gggggccaaa gacgaagtgg gctcggtgt	360
gtacacccgc ggcgtatca tccagatgtt ggacaagggtg tcaatcacta at	412

<210> 165
 <211> 361
 <212> DNA
 <213> Homo sapien

<400> 165

ttgacacccgtt gtccagcatc tgcatctgtt gagagcctca gatggctacc actaatggca	60
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gtgctaggtt ctttcaaca accagtctt gatgaaactg agagtaagag ctcaaggcca	180
gggtgtgtga ctccaaaccag taatcccaac attttaggag gctgaggcag gcagatgtct	240
tgaccccatg agtttgtgac cagcctgaac aacatcatga gactccatct ctacaataat	300
tacaaaaatt aatcaggcat tgtggatgc cctgtatcc cagatgctgg acaagggtgc	360
a	361

<210> 166
 <211> 427
 <212> DNA
 <213> Homo sapien

<400> 166

twgactgact catgtcccact acacccaaact atcttctcca ggtggccagg catgatagaa	60
tctgatcctg acttagggga atatttctt tttacttccc atcttgcattc cctgcccgtg	120

agtttcctgg ttcagggtaa gaaaggagct caggccaaag taatgaacaa atccatcctc acagacgtac agaataagag aacwtggacw tagccagcag aacmcaaktg aaamcagaac mcttamctag gatracaaamc mcrraratar ktgcycmcmc wtataataga aacccaaactt gtatctaatt aaatatttat ccacygtcag ggcattagtg gtttgataa atacgcttg gctaggattc ctgaggttag aatggaaraa caattgcamc gagggtaggg gacatgagtc aktctaa	180 240 300 360 420 427
<210> 167 <211> 500 <212> DNA <213> Homo sapien	
<220> <221> misc_feature <222> (1)...(500) <223> n = A,T,C or G	
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<210> 168 <211> 358 <212> DNA <213> Homo sapien	
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aggtagaaca aataacttctt atttttttt caccattgtg ggattggact ttaagaggtg 300
 actctaaaaa aacagagaac aaatatgtct cagttgtatt aagcacggac ccatattatc 360
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 ggaaaaactt agtcaccctg aaaacccaca aaataaataa aacttgtaga tgtggcaga 480
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 ccacatgtct cagctatattt attattttt ttatgtcat aaagtgaatc atttcttctg 660
 tattaatttc caaagggttt taccctctat ttaaatgttt tgaaaaacag tgcattgaca 720
 atgggttcat attttctt aaaaagaaaaa tataattatg aaagccaaga taatctgaag 780
 cctgtttat tttaaaaactt ttatgttct gtgggttcat ttgtttgtt gtttgggttct 840
 attttgttgg tttttactt tggtttttgt tttgtttgt tttgttttgc catactacat 900
 gcagtttctt taaccaatgt ctgtttggct aatgttaattt aagttgttta ttatgttgc 960
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 aagtttattt tttctatggc attccagcgg atattttgtt gtttgcgagg catgcgtca 1140
 atattttgtt cagttgttgc acagtattca gcaacgcctg atagtttctt tggcctttag 1200
 ttaaataaaaa agacctgttt gggatgtttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1260
 aaaaaa 1265

<210> 170
 <211> 383
 <212> DNA
 <213> Homo sapien

<400> 170

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 taatttgcattcc agagaacatg ctggctacaa ctaaaaaac cggaaaaatgtt gaatttctaa 180
 atttttcttca caaccattgtt atgcatttgc tcacagcacc acttttgcattt aataacttcag 240
 aagacaaatg tgaaaaggat aatatagtt gatcaaacaa aaacaacaca atttgcggcc 300
 ataattatca aacagcacag ctacttgcc taatttttgc gttactcaca ttgttgcgtt 360
 aacatcacac tgctcgactt aca 383

<210> 171
 <211> 383
 <212> DNA
 <213> Homo sapien

<400> 171

tgggcacctt caatatcgca agttaaaaat aatgttgcattt ttattataact tttgacctgt 60
 ttagctcaac agggtaagg catgtttaaaa atgttgcattt ctggatattt ttctttttaaa 120
 aagaacataa tgaagtaaca tttaatttgc tcaaggacta cttttgggtt aagtttataa 180
 tctagatacc tctactttt gttttgcattt ttcgcattt cacaagacc ttcagcaattt 240
 tacagggttaa aatcggttgc gtagtggagg tgaaactgaa attttttttt attctgtttt 300
 tactataggg aaagaggctg agcttgcattt cttttgggtt ttcgcattt ctgttgcattt 360
 atcatcacac tgctcgactt aca 383

<210> 172
 <211> 699
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(699)
 <223> n = A,T,C or G

<400> 172

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ggtctgcatt ctggcgccgg ctctggcca ggcctcctgg aaagttctc aggatggca	180
gcactcgtgg tgctgagcca ggcactaaat ggactgctca tgtctgctgt catggagcat	240
ggcagcagca tcacacgcct ctttgtggg tcctgctcgc tggtggtaa cgcgtgctc	300
tcagcagtcc tgctacggct gcagctcaca gccccttct tcctggccac attgctcatt	360
ggcctggcca tgcgcctgta ctatggcagc cgctagttcc tgacaacttc caccctgatt	420
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catcagcggc cctgtaacaa gtgccttg agaaaagctg gagaagttag ggcagccagg	540
ttattctctg gaggttggg gatgaagggg tacccttagg agatgtgaag tgtgggttt	600
gttaaggaaa tgcttaccat cccccccccca aaccaagtt nttccagact aaagaattaa	660
ggtaacatca atacctaggc ctgaggagc atcaccgc	699

<210> 173

<211> 701

<212> DNA

<213> Homo sapien

<400> 173

tcgggtgatg cctcctcagg ccagatcaa cttggggttg aaaactgtgc aaagaaatca	60
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cattagcagt ggaagaagaa atgttgatattttatgtcag ctatttata atcaccagag	180
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catatgagct tccatagtca ccaggacacg ggctctgaaa gtgcctcca tgcaggaca	600
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gcagtgccat cctgctgtat gcctgaggag gcatcacccg a	701

<210> 174

<211> 700

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(700)

<223> n = A,T,C or G

<400> 174

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gaaaaagacat agatttaac cggccccc tt caggagattc tgaggctcag ttcactttgt	120
tgcagttga acagaggcag caaggctagt ggttagggc acggctctta aagctgcact	180
gcctggatct gcctccccc tctgccagga accagctgcg tggccttgc ctgcgtacac	240
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tgggaggtgc tgaggtgggaa ggatcacttgc agccgggag gtggaggtg cagttagcca	540
agatcatgcc actgcactcc agcctgagta atagagtaag actctgtctc aaaaacaaca	600
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<210> 175	
<211> 484	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (484)	
<223> n = A,T,C or G	
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ccgaa	484
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<212> DNA	
<213> Homo sapien	
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gacaaatgcc aggtagcgaa attggtaactg gtccaggagt tatccaggat agatttcac	180
ccaccatggg acgtcatcgt tcaaataac tcttcaatgg ccatggggga cacatcatgc	240
ctcccacaca atcgcagttt ggagagatgg gaggcaagtt tatgaaaagc cagggctaa	300
gccagctcta ccataaccag agtcaggac tcttatccca gctgcaagga cagtcgaagg	360
atatgccacc tcggttttct aagaaaggac agcttaatgc agatgagatt agcctgagga	420
ggcatcaccc ga	432
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<211> 788	
<212> DNA	

<213> Homo sapien

<400> 177

<210> 178

<211> 786

<212> DNA

<213> Homo sapien

<400> 178

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attgttggttc gtttcttttc attaaagggtt taatcagaca gatcagacag cataattttg 180
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cactgtgcac tcttcttaggt gtaagggtat gcaactttgg atcttaaatat tctgtacaca 420
tacacacttt atatataatgt atgtatgtat gaaaacatgaa aatttagtttgc tcaaataatgt 480
gtgtgttttag tatttttagct tagtgcactt atttccacat tattttatataa attgatctaa 540
gacactttct tggtgacacc ttgaatatttgc atgttcaagg gtgcattgttgc tattccctta 600
gattgttaaa gcttaatttgc tatgatttgc tggggaaaga ttttaattttgc ccagttgcata 660
ccttctgttag tgctcgtaggg ctcttacagg gtggggaaaga ttttaattttgc ccagttgcata 720
atggacatgttgc atggcctcat tatataatgttgc gatttataagg agtttgcatttgc tgggctcaac 780
atqcta 786

<210> 179

<211> 796

<212> DNA

<213> Homo sapien

<400> 179

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acaccccccac ccgcccccttg tttggagtgc agagtttggc tttggttctt tgccttgcc 180
ggagttatact tctaattcct gttgtcctgc acaagctgaa taccgagcta cccaccgcca 240
cccaggccag gtttccactc atttattact ttatgtttctt gttccattgc tggtccacag 300
aaataaqttt tccttggag gaatgtgatt atacccttt aatttcctcc ttttgcttt 360

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tggcaatccc attaccatgc ttttttaaa aaacgtaatt tttcttgct tacattggca	480
gagtagccct tcctggctac tggcttaatg tagtcactca gtttcttaggt ggcattaggc	540
atgagacctg aagcacagac tgccttacca caaaaggtga caagatctca aaccttagcc	600
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<211> 488	
<212> DNA	
<213> Homo sapien	
<400> 180	
ggatgtgctg caaggcgatt aagttggta acgccagggt tttcccagtc acgacgttgt	60
aaaacgacgg ccagtgaatt gtaatacgc tcactatagg gcgaattggg cccgacgtcg	120
catgctcccg gccgcacatgg cgcgcggata gcatgttagg cccagacacc tgcaaggcat	180
ttggagagat tttcacgtt accagcttga tggctttt caggaggaga gacactgagc	240
actcccaagg tgaggtgaa gatttcctct agatagccgg ataagaagac taggaggat	300
gcctagaaaa tgatttagcat gcaaatttct acctgccatt tcagaactgt gtgtcagccc	360
acattcagct gcttcttgc aactgaaaag agagaggtat tgagactttt ctgtatggccg	420
ctctaacatt gtaacacagt aatctgtgtg tgggtgtgtg tgggtgtgtg tctggctca	480
acatgcta	488
<210> 181	
<211> 317	
<212> DNA	
<213> Homo sapien	
<400> 181	
tagcatgttg agcccagaca cggcgacggt acctgtatgag tgggtgtatg gcacctgtga	60
aaaggagggaa cgtcatcccc catgatattt gggacccaga tggatgaacca tggctcccg	120
tcaatgcata tttatccat gatactgtcg attgaaaggc cctgaacctg aagtttgtgc	180
tgcagggtttc tcgggactat tacctcacgg gtatcaaaa cttcctgaag gacatgtggc	240
ctgtgtgtct agtaagggat gcacatgcag tggccagtgt gcccagggtt tgggtgtgt	300
ctgggctcaa catgcta	317
<210> 182	
<211> 507	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (507)	
<223> n = A, T, C or G	
<400> 182	
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tttgggtact caggattaca gaggcatcct gtttcaggga acaaaaagat tttagctgcc	120

agcagagagc accacataca tttagaatggt aaggactgcc acctccttca agaacaggag	180
tgagggtggt ggtgaatggg aatggaaagcc tgcattccct gatgcatttg tgctctctca	240
aatcctgtct tagtcttagg aaaggaagta aagttcaag gacggttccg aactgcttt	300
tgtgtctggg ctcaacatgc tatcccgccg ccatggccgc cgggagcatg cgacgtcggg	360
cccaattcgc cctatagtga gtcgttattac aattcactgg ccgtcggttt acaacgtcgt	420
gactgggaaa accctggcgt tacccaaactt aatgccttg cagcacatcc cccttccca	480
gctggcgtaa tancggaaaag gccccca	507

<210> 183

<211> 227

<212> DNA

<213> Homo sapien

<400> 183

gatttacgct gcaacactgt ggaggttagcc ctggagcaag gcaggcatgg atgcttctgc	60
aatccccaaa tggagcctgg tatttcagcc aggaatctga gcagagcccc ctctaattgt	120
agcaatgata agttattctc tttgttcttc aacttccaa tagcctttag cttccagggg	180
agtgtcgtaa atcattacag cctggtctcc acagtgttgc agcgtaa	227

<210> 184

<211> 225

<212> DNA

<213> Homo sapien

<400> 184

ttacgctgca acactgtgga gcagattaac atcagacttt tctatcaaca tgactgggt	60
tactaaaaag acaacaaatc aatggcttca aaagtctaag gaataatttc gataattcaa	120
ctttataaaaaa cctgacaaaaa ctatcaatca agcataaaga cagatgaaga acattccag	180
attttggcca atcagatatt ttacctccac agtgttgcag cgtaa	225

<210> 185

<211> 597

<212> DNA

<213> Homo sapien

<400> 185

ggcccgacgt cgcatgctcc cggccgccat ggccgcggga ttcttaggg tctctatcca	60
ctgggaccctt taggotagtc agagtatttta gagttgagtt cttttctgtc tcccagaatt	120
tgaaagaaaa ggagttaggt gatagagctg agagatcaga tttgcctctg aagcctgttc	180
aagatgtatg tgctcagacc ccaccactgg ggcctgtggg tgaggtctgt ggcatctatt	240
tgaatgaatt gctgaagggg agcaactatgc caaggaaggg gaacccatcc tggcaactggc	300
acaggggtca ccttatccag tgctcagtc ttctttctgtc ctacctgggt ttctctcata	360
tgtgagggggc aggttagaag aagtgcctc tgttgtgcga gttttagaac atctaccagt	420
aagtggggaa gtttccacaaa gcagcagctt tgttttgtgtt atttcacct tcagtttagaa	480
gaggaaggct gtgagatgaa tgtagttga gtggaaaaga cgggtaagct tagtggatag	540
agaccctaaac gaatcactag tgcggccgccc ttgcaggtcg accatatggg agagctc	597

<210> 186

<211> 597

<212> DNA

<213> Homo sapien

<400> 186	
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accccagagg cctacagatc ctcctttagt acataagaaa atttcccaa actacctaac	180
tatatcatt tgcaagattt gtttaccaa attttgatgg cctttctgag cttgtcagtg	240
tgaaccacta ttacgaacga tcggatatta actgcccctc accgtccagg tgtagctggc	300
aacatcaagt gcagtaataa ttcattaagt tttcacctac taaggtgctt aaacacccta	360
gggtgccatg tcggtagcag atcttttagt ttgttttat ttcccataag ggtcctgttc	420
aaggtcaatc atacatgttag tgtgagcagc tagtcaactat cgcatgactt ggagggtgat	480
aatagaggcc tccttgctg ttaaagaact cttgtcccag cctgtcaaag tggatagaga	540
ccctaacgaa tcactagtgc ggccgcctgc aggtcgacca tatggagag ctc当地	597
<210> 187	
<211> 324	
<212> DNA	
<213> Homo sapien	
<400> 187	
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ccatatgttag tggatcaaga gactgcagg ccagaaagac tagccgagcc catccatgtc	120
ttccacttaa ccctgctttt ggttacacat cttaactttt ctgttcaagt ttctctgtgt	180
agtttatagc atgagtattt ggawaatgcc ctgaaacctg acatgagatc tggaaacac	240
aaacttactc aataagaatt tctccatat tttatgatg gaaaaatttc acatgcacag	300
aggagtggat agagacccta acga	324
<210> 188	
<211> 178	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(178)	
<223> n = A,T,C or G	
<400> 188	
gcgccggat tcgggggtat acctcctcat gccaaaatac aacgtntaat ttcacaactt	60
gccttccaat ttacgcattt tcaatttgc tcccccattt gttgagtcac aacaaacacc	120
attgcccaga aacatgtatt acctaacatg cacatactct taaaactact catccctt	178
<210> 189	
<211> 367	
<212> DNA	
<213> Homo sapien	
<400> 189	
tgacacccattt tccagcatct gacacagtct tggctttgg aaaatattgg ataaatgaaa	60
atgaatttct ttagcaagtgt gtataagctg agaatatacg tattcacat cctcattcta	120
agacacattc agtgcctctg aaatttagaat aggacttaca ataagtggtt tcactttctc	180
aatagctgtt attcaatttga tggtaggcct taaaagtcaa agaaatgaga gggcatgtga	240

aaaaaaagctc aacatcactg atcattagaa aacttccatt caaacccca atgagatacc	300
atctcataacc agtcagaatg gctattattha aaaagtcaaa aaataacaga tgctggacaa	360
ggtgtca	367

<210> 190
 <211> 369
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(369)
 <223> n = A,T,C or G

<400> 190

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agttttact ctggctaggc agatggtggc taaaacattc atttaccat ttattcattt	120
aattgttcct gcaaggccta tggatagagt attgtccagc actgctctgg aagctaggag	180
catggggatg aacaagatag gctacatcct gttcccacag aacttccact ttagtctggg	240
aaacagatga tatatacaaa tatataaaatg aattcaggtt gtttaagta cgaaaagaat	300
aagaaagcag agtcatgatt tanaatgctg gaaacagggg ctattgctt agatattgaa	360
ggtgcctaa	369

<210> 191
 <211> 369
 <212> DNA
 <213> Homo sapien

<400> 191

tgacaccttg tccagcatct gcacaggaa aagaaactat tatcagagtg aacaggcaac	60
ctacagaatg ggagaaaatt tttgaatct atccatctga caaaggctt atatccagaa	120
tctacaaaga acttatacaa atttacaaga aacaaacaaa caaacaactc ctcaaaaagt	180
gggtgaagga tgtgaacaga cacttctcaa aagaagacat ttatggggcc aacaaacata	240
tgaaaaaaaaag ctcatcatca ctggtaacta gataatgca aatcaaaacc acaatgagat	300
accatctcat tccagttaga atggcaatca ttaaaaagtc aggaaacaac agatgctgga	360
caaggtgtc	369

<210> 192
 <211> 449
 <212> DNA
 <213> Homo sapien

<400> 192

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caagactggc ctagtgacag tcctccagac attttttcat ttgttccata tacgtggaaat	120
ttttaaaatca tgtttcatca gtttggaaatg atttgggctg ctaatcaaca caattggatc	180
gactgttcta ctaaacaaca ggaaaaatgtg tatctggcag cctgtggaga aacactaaac	240
attgattttt ctttgcctt tacggacttt gttccagctt catgttaatac caagttctct	300
ttaagaggag aagatgttga ttttcatttgc tttctaccag actgccaccc tagtaaatat	360
tctttattta tgctggtaaa aaattgccat ccaataaga tgattcatga tactggatt	420
cctgctgagt gtcaagtggc caagcgtca	449

<210> 193	
<211> 372	
<212> DNA	
<213> Homo sapien	
<400> 193	
tgacgcttgg ccacttgaca ccagggatgt akcagttgaa tataatcctg caattgtaca	60
tattggcaat ttcccatcaa acattctaga aagagacaac caggattgct aggccataaa	120
agctgcaata aataactggt aattgcagta atcatttcag gccaattcaa tccagttgg	180
ctcagaggtg ctttggctg agagaagagg tgagatataa tgtgtttct tgcaacttct	240
tggaagaata actccacaat agtctgagga ctagatacaa acctatttc cattaaagca	300
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ggccaagcgt ca	372
<210> 194	
<211> 309	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (309)	
<223> n = A,T,C or G	
<400> 194	
tgacgcttgg ccacttgaca cttatgtaga atccatcggt ggctgatgca agccctttat	60
ttaggcttag tgggtgggc accttcaata tcacactaga gacaaacgcc acaagatctg	120
cagaaacatt cagttctgan cactcgaatg gcaggataac ttttgtgtt gtaatccttc	180
acatatacacaa aaacaaaactc tgcantctca cgttacaaaa aaacgtactg ctgtaaaata	240
ttaagaaggg gtaaaggata ccatctataa caaagtaact tacaactagt gtcaagtggc	300
caagcgtca	309
<210> 195	
<211> 312	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (312)	
<223> n = A,T,C or G	
<400> 195	
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ggactgcaac tatccccact tcccagatga ggggaccaan gtacacatta ggaccggat	120
gggagcacag atttgcgttccga tcccagactc caagcactca gcgtcactcc aggacagcgg	180
ctttcagata aggtcacaaaa catgaatggc tccgacaacc ggagtcaagt cgtgctgagt	240
taaggcaatg gtgacacgga tgcacgtgtt acctgtaatg gttcatcgta agtgtcaagt	300
ggccaagcgt ca	312

<210> 196		
<211> 288		
<212> DNA		
<213> Homo sapien		
<400> 196		
tgtatcgacg tagtggtctc ctcagccatg cagaactgtg actcaattaa acctcttcc	60	
tttatgaatt acccaatctc gggtagtgtc tttatagtag tgtgagaatg gactaataca	120	
agtacatttt acttagtaat aataataaaac aaatataatta cattttgtg tatttactac	180	
accatatttt ttattgttat tgttagtgc accttctact tattaaaaga aataggcccg	240	
aggcgggcag atcacgaggt caggagatgg agaccactac gtcgatac	288	
<210> 197		
<211> 289		
<212> DNA		
<213> Homo sapien		
<400> 197		
ttgggcaccc tcaatatcat gacaggtat gtgataacca agaaggctac taagtgatta	60	
atgggtgggt aatgtataca gagtaggtac actggacaga ggggttaattc atagccaagg	120	
caggagaagc agaatggcaa aacatttcat cacactactc aggatagcat gcagttaaa	180	
acctataagt agtttatttt tggaaatttc cacttaatat tttcagactg caggttaacta	240	
aactgtggaa cacaagaaca tagataaggg gagaccacta cgtcgatac	289	
<210> 198		
<211> 288		
<212> DNA		
<213> Homo sapien		
<400> 198		
gtatcgacgt agtggtctcc caagcagtgg gaagaaaacg tgaaccaatt aaaatgtatc	60	
agataccccca aagaaaggcg cttgagtaaa gattccaagt gggtcacaat ctcagatctt	120	
aaaattcagg ctgtcaaaaga gatttgctat gaggttgc tcaatgactt caggcacagt	180	
cgcgaggaga ttgaaggccct ggccattgtc aagatgaagg agctttgtgc catgtatggc	240	
aagaaagacc ccaatgagcg ggactcctgg agaccactac gtcgatac	288	
<210> 199		
<211> 1027		
<212> DNA		
<213> Homo sapien		
<220>		
<221> misc_feature		
<222> (1) ... (1027)		
<223> n = A,T,C or G		
<400> 199		
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aancccgagg tttccccatt cagggaggtg taaaaagncc gcccaggat tgtaanagga	120	
ttcaataata gggggatgg gcccngaagt tgcaaggtc cngcccgcca tgnccgcggg	180	
atttagtgac attacgacgs tggtaataaa gtggsccaa waaatattt tgatgtgatt	240	

tttsgaccag tgaacccatt gwacaggacc tcatttccty tgagatgrta gccataatca	300
gataaaagrt tagaagtytt tctgcacgtt aacagcatca ttaaatggag tggcatcacc	360
aatttcaccc tttgttagcc gataccttcc ccttgaaggc attcaattaa gtgaccaatc	420
gtcatacggag agggatggc atggggattt atgatgatat caggggtgat accttcacag	480
gtgaaaggca tattcttgc tctatactga ataccacaag taccctttt accatgtcga	540
ctagcaaatt tttatccat ctgtgtwac cctaacagag cgtaccctt ttttacaaaa	600
tttatacct tcctgattga gagttaccat aacctgatcc acaatgccc tctcgctwgt	660
tctgagaaaa gtgctacagt ctcttgcgtt atagcgtcta ttggtgctct ccaattcatc	720
ttcattttt aggcaagggtg aactgttttgc cctataataa cmtcatctcc tgatacmcg	780
aacccckgga rctatcaaac catcatcatc cagcgttckt watgtymcta aatccctatt	840
gcggccgcct gcaggtcaac atatngaaa accccccacc ccttnggagc ntaccttgaa	900
ttttccatat gtcccntaaa ttanctngnc ttanctngc cntaacctnt tccggttaa	960
attgtttccg ccccnnttcc cncccttnna accggaaacc ttaattttna accnngggtt	1020
cctatcc	1027
<210> 200	
<211> 207	
<212> DNA	
<213> Homo sapien	
<400> 200	
agtgacattt ctagggcat gaagttgccc cttttttttt tttttttttt tttttttttt	60
cacttggta agcctgatcc ctctggttt tcacaaagaa taggtggaa taaagaaaagt	120
ggacacttaa ataagctata aattatatgg tcttgcgttgc gcaggagaca actgcacagg	180
tatactacca gcgtcgtaat gtcacta	207
<210> 201	
<211> 209	
<212> DNA	
<213> Homo sapien	
<400> 201	
tgggcacccat caatatctat taaaaggcaca aataactgaag aacacaccaa gactatcaat	60
gagggttacat ctggagtccct cgatatatca ggaaaaatgg aagtgaacat tcacagagtt	120
ttacttcttt gggaaactcaa atgctagaaa agaaaagggt gcccttttc tctggcttcc	180
tggtcctatc cagcgtcgta atgtcacta	209
<210> 202	
<211> 349	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(349)	
<223> n = A,T,C or G	
<400> 202	
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tcactgaaca caccgaagac cgtggatgg taaccgttca cagtaatcgt tccagtcgtc	120
tgcgggaccc cgacgagcgt cactgggtac agaccagatt cagccggaag agaaagcgcc	180

gcagggagag actcgaactc cactccgctg gtgagcagcc ccatgtttc aactcgaagt	240
tcaaacggca ttgggttata taccatcagc tgaacttcac acacatctcc ttgaacccac	300
tggaaatcta ttttcttgtt cgcgttccctt ccacagtgtt gcagcgtaa	349

<210> 203
 <211> 241
 <212> DNA
 <213> Homo sapien

<400> 203	
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cagtttcaa cgcaatatag tatagttat ctgattctt tgatctccag gacactttaa	120
acaactgcta ccaccaccac caaccttaggg atttaggatt ctccacagac cagaaattat	180
ttctcctttt agtttcaggc tcctctggta ctccgttca tcaatgggtg gtaaatggct	240
a	241

<210> 204
 <211> 248
 <212> DNA
 <213> Homo sapien

<400> 204	
tagccattta ccaccatct gcaaaccswg acmwwcargr cywgcwackya ggcgatttga	60
agtactggta atgctctgat catgttagtt acataagtgt ggtcagttt caaaaattca	120
cagaactaaa tactcaatgc tatgtgttca tgtctgtt tatgtgtgtg taatgtttca	180
attaagtttt tttaaaaaaaa agagatgatt tccaaataag aaagccgtgt tggttaaggca	240
agaggagc	248

<210> 205
 <211> 505
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(505)
 <223> n = A,T,C or G

<400> 205
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 ctctaatact ggtatgcta gaggtgatgt ttttggtaaa caggcggtt aagatttgc
 gagttccctt tactttttt aaccttcct tatgagcatg cctgtgttgg gttgacagtg
 gggtaataa tgacttggta gttgattgta gatattgggc tgttaattgt cagttcagtg
 ttttaatctg acgcaggcatt atgcggagga gaatgtttc atgttactta tactaacatt
 agttcttcta taggggtgata gattggtcca attgggtgtg aggagttcag ttatatgttt
 gggattttt aggttagtggg tggtaatgtt gacgcgttca ttaattgggtg gctgcttt
 rgcctactat ggggtggtaaa tggct

<210> 206
 <211> 179

<212> DNA		
<213> Homo sapien		
<400> 206		
tagactgact catgtcccct accaaagccc atgtaaggag ctgagttctt aaagactgaa	60	
gacagactat tctctggaga aaaataaaat ggaattgta cttaaaaaaa aaaaaaaatc	120	
ggccgggcat ggtacacac acctgtaatc ccagctacta gggacatga gtcagtcta	179	
<210> 207		
<211> 176		
<212> DNA		
<213> Homo sapien		
<400> 207		
agactgactc atgtcccta ccccaccttc tgctgtgctg ccgtgttctt aacaggtcac	60	
agactggtagc tggtagtgg cctgggggtt gggacactt attatatggg atacaattt	120	
aggagttgga attgacacga tttagtgact gatggatat gggtagtaaa tggcta	176	
<210> 208		
<211> 196		
<212> DNA		
<213> Homo sapien		
<400> 208		
agactgactc atgtcccta tttaacaggg tctctagtgc tgtaaaaaaa aaaaatgctg	60	
aacattgcat ataacttata ttgtaaaaa tactgtacaa tgactttattt gcatctgggt	120	
agctgttaagg catgaaggat gccaagaat ttaaggaata tgggtggtaa atggctaggg	180	
gacatgagtc agtcta	196	
<210> 209		
<211> 345		
<212> DNA		
<213> Homo sapien		
<220>		
<221> misc_feature		
<222> (1)...(345)		
<223> n = A,T,C or G		
<400> 209		
gacgcttggc cacttgacac cttttattt ttaaggattc ttaagtcatt tangtnactt	60	
tgtaagtttt tcctgtcccc ccataagaat gatacttta aaaattatgc tgggttagca	120	
aagaagatac ttctagctt agaatgtgta ggtatagcca ggattctgtt gaggaggggt	180	
gatttagagc aaatttctta ttctccttgc ctcatctgta acatggggat aataatagaa	240	
ctggcttgcac aagggtggaa ttagtattac atggtaaata catgtaaaat gtttagaatg	300	
gtgccaagta tcttaggaatg acttggcat gggtagtaaa tggct	345	
<210> 210		
<211> 178		
<212> DNA		
<213> Homo sapien		

<400> 210		
gacgcttggc cacttgacac tagagtaggg tttggccaac tttttctata aaggaccaga	60	
gagtaaatat ttcaaggctt gtgggttgtg cagtcctct tgcaactact cagctctgcc	120	
attgttagcat agaaaatcagc catagacagg acagaaaatga atgggtggta aatggcta	178	
<210> 211		
<211> 454		
<212> DNA		
<213> Homo sapien		
<400> 211		
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caccacttgc tgtttttgc catgtataacc aagtagcagt ggtgtgaggc catgttgc	120	
ttttgattcg atatcagcac cgtataagag cagtcttgc gccattaatt tatcttcatt	180	
gtagacagca tagttagag tggatctcc atactcatct ggaatatttg gatcagtgc	240	
atgttccagc aacattaacg cacattcatc ttccctggcat tgcacggct ttgtcagagc	300	
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<223> n = A,T,C or G	

<400> 232	
tgctcctctt gccttaccaa ccacaaattha gaaccataat gagatgtcac ctcatacctg	60
gtgggattaa cattattha aaaatcagaa gtattgacaa ggatgtgaag aaattagaac	120
atctgtgcac tggtggggg aatgtaaaaa aggtgtggcc actatggta acagcatgaa	180
ggttcctcaa aaaaattht tttatcta ctctatgatc gatcttgagg ttgttatgc	240
aaaagaactg aaatcaggat ttgaggaaa tattcacatt cccacatcca tttctgctt	300
attcataata ctcaagagat gaaacaacc taaatgtcca tcccggatg aatggataaa	360
cacagtgtgg tatatgcata caatggaata ttatttagtc tttaaaaaga aaaattctat	420
catatactac aacttanatn aacttgagg acacaatgct nagtgaata agccacggaa	480
ggacgaataac tgcatatttc ctttatatga agtataaaa gtgtcaaac tcttanagca	540
naaagtaaaa atgggtggtt gccanacagt tggttagcn agaaganaan cctant	596
<210> 233	
<211> 96	
<212> DNA	
<213> Homo sapien	
<400> 233	
tcttcgaag accttcgcg actcttaagc tcgtggggtaaggcaaga ggagcggtgg	60
taaggcaaga ggagcggtgg taaggcaaga ggagca	96
<210> 234	
<211> 313	
<212> DNA	
<213> Homo sapien	
<400> 234	
tgtaagtcga gcagtgtgat gataaaactt gaatggatca atagttgctt cttatggatg	60
agcaaagaaa gtagttctt gtgatggat ctgctctgg caaaaatgct gtgaacgttg	120
ttgaaaagac aacaaagagt ttagagtagt acataaattt agaatagtagc ataaacttag	180
aatagtagcat aaacttagta cataaataat gcaccaagca ggggcaggc ttgagagaat	240
tgacttcaat ttggaaagag tatctactgt aggttagatg ctctcaaaca gcatcacact	300
gctcgactta caa	313
<210> 235	
<211> 550	
<212> DNA	
<213> Homo sapien	
<400> 235	
aacgaggaca gatccttaaa aagaatgtt agtggaaaaa gtagaaaata agataatctc	60
caaagtccag tagcattatt taaacatttt taaaatatac actgataaaa attttgtaca	120
tttcccaaaa atacatatgg aagcacagca gcatgaatgc ctatggrrt gaggataggg	180
gttggggta gggatggggta aaaaaggaaa aaataaaacc agagaggagt cttacacatt	240
tcatgaacca aggagtataa ttatttcaac tatttgtacc wgaagtccag aaagagtgg	300
ggcagaagggg ggagaagagg gcgaagaaac gttttgggta gagggtccc asaagagaga	360
tttgcgtat gtggcgctac atacgtttt ccagatgcc ttaagctctg caccctattt	420
ttctcatcac taatattaga ttaaaccctt tgaagacagc gtctgtggtt tctctacttc	480
agctttccct ccgtgtcttg cacacagtag ctgtttaca agggttgaac tgactgaagt	540
gagattattc	550

<210> 236	
<211> 325	
<212> DNA	
<213> Homo sapien	
<400> 236	
tagactgact catgtccctt accagagtag ctagaattaa tagcacaagc ctctacaccc	60
aggaactcac tattgaatac ataaatggaa tttattcagc cttaaaaagt ttggaaggaa	120
attctgacat atgctaaaac atggatgaac cttgaagact ttatgataag taaaagaagc	180
cagtcataaa aggaaaaata ttgcatgatt ccacttatac gaggtaccta gagtagtcaa	240
tttcatagaa acacaaaata gaatgggttt tgccaggct tttgaggaaa aggaaatgac	300
aagtttaggg acatgagtca gtcta	325
<210> 237	
<211> 373	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(373)	
<223> n = A,T,C or G	
<400> 237	
tagactgact catgtccctt atctactcaa catttccact tgaagtctga taggcacatctc	60
agacttatct tgcctccaaag caaactctttt attttttttc atcctagtttct ttatttcttg	120
tgctgtctta cccatctcaa aagagtgcctt aaatccacca agttgctgaa acagaaatct	180
aagaaaatatc cttgattctt cttttccca tctacttcac ttcttaattca ttatgtaaata	240
atctgtttca gaaaacccaaa cacctcatgt tctcactcat aagggggagt tgaacaatga	300
gaacacacacag acacagggag gggaaacatca cacaccacgg cccgtcaggg agtangggac	360
atgagtcatgt cta	373
<210> 238	
<211> 492	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(492)	
<223> n = A,T,C or G	
<400> 238	
tagactgact catgtccctt ataatgctcc caggcatcag aaagcatctc aaactggagc	60
tgacaccatg gcagagggttt caggttaagtc acaaaaagggg tcctaaagaa tttgcctca	120
atatacagagt gattagaaga agtggacaga gctacccaaat taaaacatat gcgagataaa	180
aaaaatatgg cacttgcata cacacactac aggagggaaaa taaggaacat aatagcatat	240
tgtgctatta tgatgatgaa gaacctctt anaagaaaac ataaccaaag aaacaaagaa	300
aattcctgcn aatgtttat gctatagaag aaattaacaa aaacatataat tcaatgaatt	360
cagaaaagtt agcaggtcan aagaaaacaa atcaaagacc agaataatcc catttttagat	420

tgtcgagtaa	actanaaacag	aaagaatacc	actggaaatt	gaattcctac	gtangggaca	480
tgantcantc	ta					492
<210> 239						
<211> 482						
<212> DNA						
<213> Homo sapien						
<220>						
<221> misc_feature						
<222> (1)...(482)						
<223> n = A,T,C or G						
<400> 239						
tggaaagtat	ttaatgatgg	gcaacttgct	gtttacttcc	tacatatccc	atcatcttct	60
gtatTTTTT	aaataacttt	tttttgaggatt	tttaaagtaa	ccttattctg	agaggtaaca	120
tggattacat	acttctaagc	cattaggaga	ctctatgtta	aacccaaaagg	aaatgttact	180
agatcttcat	ttgatcaata	ggatgtgata	atcatcatct	ttctgctcta	atggaaaagt	240
actanaaaaca	tggaaccata	atcttagatg	aacaacgtta	gaatttgcac	taattctacg	300
gaatttcagt	aattcggcaa	atgtcgggca	gtgacacaac	atttcatgac	ggggacgcat	360
ctaccaactt	ctggcgataa	gggccaccct	tcctctgtta	cttacagtcc	catttcatac	420
acagtctttg	attaaatatt	cacattttt	ctctacctaa	agaccttcaa	gaccagtacg	480
ta						482
<210> 240						
<211> 519						
<212> DNA						
<213> Homo sapien						
<220>						
<221> misc_feature						
<222> (1)...(519)						
<223> n = A,T,C or G						
<400> 240						
tgtatcgacg	tagtggtctc	cccatgtat	agtctgaaat	atagcctcat	gggatgagag	60
gctgtcccc	agcccgacac	cgtaaaggg	tctgtctga	ggtggattag	taaaagagga	120
aaggccttgc	gttggatag	aggaaggca	ctgtctcctg	cctgcccc	ggaactgaat	180
gtctcggtat	aaaacccat	tgtacattt	ttcaattctg	agataggaga	aaaaccaccc	240
tatggcggga	ggcgagacat	gttggcagca	atgctgcctt	gttatgctt	actccacaga	300
tgtttggcgc	gaggaaaaca	taaatctggc	ctacgtgcac	atccaggcat	agtacccc	360
tttgaactta	attatgacac	agattcctt	gctcacatgt	tttttgcgt	accttctcct	420
tattatcacc	ctgctctcct	accgcattcc	ttgtgctgag	ataatgaaaa	taatatcaat	480
aaaaacttga	nggaactcgg	agaccactac	gtcgataca			519
<210> 241						
<211> 771						
<212> DNA						
<213> Homo sapien						
<220>						

<221> misc_feature
 <222> (1)...(771)
 <223> n = A,T,C or G

<400> 241

tgtatcgacg tagtgttctc cactccggcc ttgacggggc tgctatctgc cttccaggcc	60
actgtcacgg ctccgggta gaagtcaatt atgagacaca ccagtgtggc cttgttggct	120
tgaagctcct cagaggaggg tgggaacaga gtgaccgagg gggcagcctt gggctgacct	180
aggacggtca gcttggtccc tccgccaaac acgagagtgc tgctgcttgt atatgagctg	240
cagtaataat cagcctcgtc ctcagcctgg agccagaga tggtcaggga ggcgtgttg	300
ccanacttgg agccagagaa gcgattagaa acccctgagg gccgattacc gacctcataa	360
atcatgaatt tgggggctt gcctgggtgc tgttgttacc angagacatt attataacca	420
ccaacgtcac tgctggttcc antgcagggaa aatgggtga tcnaactgtc caagaaaacc	480
actacgtcca taccaatcca ctaattgcn gcccctgca ggttcaacca tattggggaa	540
naactcccn cgcgcgtttg gattgnat naaccttga aatttttcc tattanttgt	600
ccccctaaaaaa taaaccnntg gcnnttaatc cattgggtcc atanctntt tncccggtt	660
ttaaaanttg ttatcccgc cncccnattt ccccccaac tttccaaaac ccgaaaccnt	720
tnaaatttnt tnaaaccctg gggggttccc nnaatnnan ttinaanctnc c	771

<210> 242

<211> 167

<212> DNA

<213> Homo sapien

<400> 242

tgggcacctt caatatcggtt ctcatcgata acatcacgct gctgatgtc ctgttgcgtgg	60
tcctctctag gaacctctgg attttcaat tcttgagga attcatccaa attatctgcc	120
tctcctcctt tcctcctttt tctaaggctc tctggtacaa gcggtca	167

<210> 243

<211> 338

<212> DNA

<213> Homo sapien

<400> 243

ttgggcaccc tcaatatcta ctgatctaaa tagtgtggtt tgaggcctct tgttcctggc	60
taaaaatcct tggcaagagt caatctccac tttacaatag aggtaaaaat cttacaatgg	120
atattcttga caaagcttagc atagagacag caattttaca caaggtattt ttcacctgtt	180
taataacagt ggtttccta caccatagg gtgcaccaa gggaggagtg cacagttgca	240
gaaacaaatt aagatactga agacaacact acttaccatt tcccgtatag ctaaccacca	300
gttcaactgt acatgtatgt tcttatgggc aatcaaga	338

<210> 244

<211> 346

<212> DNA

<213> Homo sapien

<400> 244

tttttggctc ccatacagca cactctcatg ggaaatgtct gttctaaggtaa caaccataaa	60
tgcaaaaatc atcaatatac ttgaagatcc ccgtgttaagg tacaatgtat ttaatattat	120
cactgataca attgatccaa taccagttt agtctggcat tgaatcaaact cactgtttt	180

gttgttaaaa aagagaaaata tttagcttat attaagtac catattgtaa gaaaaaaagat
 gcttatcttt acatgctaaa atcatgatct gtacattggc gcagtgaata ttactgtaaa
 agggagaag gaatgaagac gagctaagga tattgaaggt gccccaa 346

<210> 245
 <211> 521
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(521)
 <223> n = A,T,C or G

<400> 245 60
 accaatccca cacggatact gagggacaag tatatcatcc catttcattcc ctacagcagc
 aacttcatga ggcaggagtt attagtcggc ttttacagaa gaggaaactg agacttaggg
 agatcaagta atttgcggcag gtgcacaaat tagtgataga gccaggggctt gaagcgcacgt
 ctgtcttaag ccaatgaccc ctgcagattt ttagagcaac tgttctccac aacagtgtaa
 gcctcttgct anaagcttagt gtccacaagg gcagagattt ttgtctgttt tgctcattgc
 tccttccccca ttgcttagag cagggtctgc cacgaancag gttctcaatg catagttatt
 aaatgtatat aagagcaaac atatgttaca gagaactttc tttatgtttc tcacttacat
 gaatcacctg tganatgggt atgctgttc cccantgttg cagatnaaga tattgaangt
 gcccaaataca ctanttgcgg ggcgcctgcan gtccancata t 120
 180
 240
 300
 360
 420
 480
 521

<210> 246
 <211> 482
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(482)
 <223> n = A,T,C or G

<400> 246 60
 tggAACCAAT ccaaataccca atcaatgata gactggataa agaaaatttg gcacatgttc
 accatgaaat actatgcagc catabaaaag gatgagttca tattttgc agggacatgg
 atgaagctgg agaccatcat tctcagcaaa ctaacaagg aacagaaaac caaacactgc
 atgttctcac tcttaagtgg gagctgaaca atgagaacac atggacacag ggaggggaac
 atcacacagt gggcctgct ggtggtagg ggtctagggg agggatagca ttaggagaaa
 tacctaattgt agatgacggg ttgatgggtc cagcaaacca ccatgacacg tttatgttca
 tttatgttca ctcacatgttcc ccccagaact taaatgttta ataaaaaaat
 taagaaaaaa gttaaatgttca tcatagatac ataaaaatattt gttatgttca aaggtgc
 aa 482

<210> 247
 <211> 474
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(474)
 <223> n = A,T,C or G

<400> 247

ttcgatacag gcacagagta agcagaaaaa tggctgtgg ttaaccaagt gagtacagtt	60
aagtgagaga ggggcagaga agacaaggc atatgcaggg ggtgattata acaggtggtt	120
gtgctggaa gtgagggta tcggggatga ggaacagtga aaaagtggca aaaagtggta	180
agatcagtga attgtacttc tccagaattt gatttctggn ggagtcaa atactatccag	240
tttgggtat catangcaa cagttgaggt ataggaggt gaagtcncag tggataatt	300
gaggttatga anggtttggt actgactggt actgacaang tctgggtat gaccatggg	360
atgaatgact gtanaagcgt anaggatgaa actattccac ganaaagggg tccnaaaact	420
aaaaannnaa gnnnnngggg aatattattt atgtggatat tgaangtgcc caaa	474

<210> 248

<211> 355

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(355)

<223> n = A,T,C or G

<400> 248

ttcgatacag gcaaacatga actgcaggag ggtgggtgacg atcatgatgt tgccgatgg	60
ccggatggnc acgaagacgc actggancac gtgcctacgt cctttgctc tggtgatggc	120
cctgagggga cgcaggaccc ttatgaccct cagaatctc acaacgggag atggcactgg	180
attgantccc antgacacca gagacacccc aaccaccagn atatcantat attgtatgtag	240
ttcctgtaga nggccccctt gtggaggaaa gtcctatnag ttggcatct tcaacaggat	300
ctcaacagtt tccgatggct gtgatggca tagtcatant taaccntgtn tcgaa	355

<210> 249

<211> 434

<212> DNA

<213> Homo sapien

<400> 249

ttggattggc cctccaggag aacaaggggaaaaggtgac cgagggctcc ctggactca	60
aggatctcca ggagcaaaag gggatgggg aattcctggt cctgctggc ccttaggtcc	120
acctggcctt ccaggcttac caggtcctca aggccaaag ggtacaaaag gctctactgg	180
acccgctggc cagaaagggtg acagtggct tccagggcct cctggccctc caggtccacc	240
tggtaagtc attcagcctt taccaatctt gtcctccaaa aaaacgagaa gacatactga	300
aggcatgcaa gcagatgcag atgataatat tcttgattac tcggatggaa tggaagaaat	360
atttggttcc ctcaattccc tgaaacaaga catcgagcat atgaaatttc caatgggtac	420
tcagaccaat ccaa	434

<210> 250

<211> 430

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(430)

<223> n = A,T,C or G

<400> 250

tggattggtc acatggcaga gacaggattc caaggcagtg agaggaggat acaatgcttc	60
tcactagtta ttattattta ttttattttt gagatgaagt ctcgctttgt ctcccaggct	120
ggagagcgggt ggtgcgatct tggctctcg caaccccgcc ctcaagcaat tctcctgtct	180
tagcctcgcg ggttagatgga attacaggcg cccacccgcca tgcccaacta atttttttgt	240
gtcttcagta gagacagggt ttgcgcatgt tggcaggct ggtcttgaac tcctgacctc	300
nagtgatctg ccctcctcg cctcacaag tgctggaatt acaggcatgg gctgctgcac	360
ccagtcaact tctcaactgt tatggcctta tcattttcac cacattctat tggcccaaaaa	420
aaaaaaaaaaan	430

<210> 251

<211> 329

<212> DNA

<213> Homo sapien

<400> 251

tggtaactcca ccatyatggg gtcaaccggcc atcctcgccc tcctcctggc tgttctccaa	60
ggagtctgtg ccgaggtgca gtcgrtgca gtcggaggag aggtaaaaaa gtccggggag	120
tctctgaaga tctcctgtaa gggttctgca tacacctta agatctactg gatccctgg	180
gtgcgccagt tgcccgaa aggctggag tggatgggc tcatcttcc tgatgactct	240
gataccagat acagcccgta cttccaaggc caggtcacca tctcagtcga taagtccatc	300
agcaccgcct atctgcagtg gactacaa	329

<210> 252

<211> 536

<212> DNA

<213> Homo sapien

<400> 252

tggtaactcca ctcagccaa ccttaattaa gaattaagag ggaacctatt actattctcc	60
caggctcctc tgctctaacc aggcttctgg gacagtatta gaaaaggatg tctcaacaag	120
tatgttagatc ctgtactggc ctaagaagtt aaactgagaa tagcataaat cagaccaaac	180
ttaatggtcg ttgagacttg tgcctggag cagctggat aggaaaactt ttggcagca	240
agaggaagaa ctgcctggaa gggggcatca tgtaaaaaat tacaagggaa acccacacca	300
ggcccccttc ccagctctca gcctagagta ttgcatttc tcagcttagag actcacaact	360
tccttgctta gaatgtgcca cggggggag tccctgtgg tgatgaggct ctcaagagtg	420
agagtggcat cctatcttct gtgtgccac aggacgtgg cccgagactt agcaggtgaa	480
gtttctggtc caggcttgc cttgactca ctatgtgacc tctggggag taccaa	536

<210> 253

<211> 507

<212> DNA

<213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(507)
 <223> n = A,T,C or G

<400> 253

ntgttgcgat	cccagtaact	cgggaagctg	aggcgggagg	atcacctgag	ctcaggaggt	60
tgaggccgca	gtgagccggg	accacgcccac	tacactccag	cctggggcat	agagttagac	120
cctccaagac	agaaaaagaaa	agaaaaggaaag	ggaaaaggaa	agggaaaagg	aaaaggaaaa	180
ggaaaaggaa	aagaaaaaga	caagacaaaa	caagacttga	atttggatct	cctgacttca	240
attttatgtt	ctttctacac	cacaattcct	ctgcttacta	agatgataat	ttagaaaccc	300
ctcggtccat	tcttacagc	aagcttggaa	tttggtcaag	taattacaat	aatagtaaca	360
aatttgaata	ttatatgcca	gtgttttc	attcctgctc	tcacttaatt	ctcaccactc	420
tgatataaaat	acaatttgcg	ccgggtgtgg	tggctcatgc	ctgtaatccc	ggcactttgg	480
gagaccgagg	ttggccgat	gcaacaa				507

<210> 254

<211> 222

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(222)

<223> n = A,T,C or G

<400> 254

ttggatttgt	cactgtgagg	aagccaaatc	ggatccgaga	gtcttttct	aaaggccagt	60
actggccaca	cttttcctg	cgccttcct	caaagctgaa	gacacacaga	gcaaggcgct	120
tctgtttac	tcccaatgg	taactccaa	ccatagatgg	ttagctnccc	tgctcatctt	180
tccacatccc	tgcttattcag	tatagtcgt	ggaccaatcc	aa		222

<210> 255

<211> 463

<212> DNA

<213> Homo sapien

<400> 255

tgttgcgatc	cataaatgct	gaaatggaaa	taaacaacat	gatgagggag	gattaagtt	60
gggagggagc	acattaaggt	ggccatgaag	tttggggaa	gaagttagctt	ttgaacaagg	120
ccttgggttt	aagagctgtat	gagagtgtcc	cagacagagg	ggccacttgg	acaatagacg	180
agatgggaga	gggcttggaa	ggtgtcgaa	atagaagga	ttttgttctg	gtatgagtct	240
agtgaacaca	gaggcgagag	gccctgggg	gtgcagctgg	agagttatgc	agaataacat	300
taggccctgt	gggggactgt	agactgtca	caataatcca	cagttggat	tttattctaa	360
gagtgtatgg	aagccgtgga	aagggggta	agcaaggagt	gaaattatca	gatttacagt	420
gataaaaata	aattggctcg	gctactgggg	aaaaaaaaaa	aaa		463

<210> 256

<211> 262

<212> DNA

<213> Homo sapien

<400> 256
 ttggatttgtt caacctgctc aactctacyt ttccctccttc ttccctaaaaa attaatgaat
 ccaatacatt aatgcacaaa ccctgggtt ttatcaatat ttctgttaaa aagtattatc
 cagaactgga cataatacta cataataata cataacaacc cttcatctg gatgcaaaca
 tctattaata tagcttaaga tcactttcac ttacagaag caacatcctg ttgatgttat
 tttgatgttt ggaccaatcc aa

60
 120
 180
 240
 262

<210> 257
 <211> 461
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(461)
 <223> n = A,T,C or G

<400> 257
 gnggnnnnnn nnncattcg actcngttcc cttgtancc ggtcgacatg gccgcgggat
 taccgcttgt nnctgggggt gtatggggga ctatgaccgc ttgttagctgg gggtgtatgg
 gggactatga ccgctttagt mtggkgtgt atgggggact atgaccgctt gtcgggtggt
 cgataaaaacc gacgcaagggg acgtgatcga agctgcgttc ccgctcttc gcatcggtag
 ggtatcatgga cagcaatatac cgcatcgyc tgaaggcgtt cgaccatcgc gtgctcgatc
 aggcgaccgg cgacatcgcc gacaccgcac gccgtacccgg cgcgctcatc cgcggtccga
 tcccgcttcc cacgogcatac gagaagttca cggtaaccgg tggcccgac gtcgacaaga
 agtcgacgca gcagttcgag gtgcgtacct acaagcggtc a

60
 120
 180
 240
 300
 360
 420
 461

<210> 258
 <211> 332
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(332)
 <223> n = A,T,C or G

<400> 258
 tgaccgcttg tagctggggg tttatggggg actacgacccg cttgttagctg ggggtgtatg
 gggactatg accgcttgc gctgggggtg tatgggggac tatgaccgct ttttagctgg
 ggtgtatggg ggactaggac cgctttagc tgggggtgtt tggggacta tgaccgcttg
 tagctggggg tttatggggg actacgacccg cttgttagctg ggggtgtatg gggactatg
 accgcttgc nctgggggtg tatgggggac tatgaccgct tttgtgtgcct gggggatggg
 aggagagttt tggttggggaa aaaaaaaaaaa aa

60
 120
 180
 240
 300
 332

<210> 259
 <211> 291
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(291)
 <223> n = A,T,C or G

<400> 259
 taccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt 60
 gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt gaccgcttgt 120
 gaccgcttgt gaccgcttgt nacngggggt gtctggggga ctatganna ntgtactgg 180
 ggggtctgg gggncatga nngantgtna cnggggggtgt ctgggggact atganngact 240
 gtgcnnctg ggggatcnga ggagantnngn ggntagngat ggttngggan a 291

<210> 260
 <211> 238
 <212> DNA
 <213> Homo sapien

<400> 260
 taagagggta ctggtaaaa tacaggaat ctgggtaat gaggcagaga accaggatac 60
 tttgaggtca gggataaaaa ctagaatttt tttctttttt tttgcctgag aaacttgctg 120
 ctctgaagag gcccattgtat taattgtttt gatttcctt ttcttacagc ccttcaagg 180
 gcagagccct ccttattcctg aaggaatctt atccttagct atagttatgta ccctctta 238

<210> 261
 <211> 746
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(746)
 <223> n = A,T,C or G

<400> 261
 ttgggcacct tcaatatcaa tagctaacat ttattgagtg tttatcgat cataaaacac 60
 tgttctaaggc cttaaacgt actaattcat ttaatgctca taatcacttt agaagggtggg 120
 tactagtatt agtctcattt acagatgcaa catgcaggca cagagaggaa aattaacttg 180
 cccaaaggtaa cacagctaag aaatagaaaa aatattgaat ctggaaagtt gggcttctgg 240
 gtaacccaca gagtcttcaa tgagcctggg gcctcactca gtttgccttt acaaagcgaa 300
 tgagtaacat cacttaattt agtgatgttgg ccaaattggag gtcagctacg agtttctgt 360
 gttcttgcag tggactgaca gatgtttaca acgtctggcc atcagtwaat ggactgatta 420
 tcattggaw gtgggtgggc tgaatgttgg ccagtgaaat ttattcawgc catatttta 480
 tgtttagat gacttttggc tggtcctagg gcaagctctg tctgscacgg aacacagaat 540
 wacacaggga ccccccataat ttctgggtgtg gctagaacca tgaaccactg gttgggggaa 600
 caagcggtaa aaacctaagt gcccggct ggcagggtcc acccatatgg ggaaaactcc 660
 cnacgcgttt ggaatgcctn agctngaaatt attctaanaat ttgtccncnt aaaatttagcc 720
 tggcgtaa tcangggtn naagcc 746

<210> 262
 <211> 588
 <212> DNA

<213> *Homo sapien*

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<220>
<221> misc_feature
<222> (1)...(588)
<223> n = A, T, C or
```

<400> 262

tgaccgcctg	tcatctcaca	tggggcctcg	cacgcttttgc	cttttgttagg	aaacctgaca	60
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ttgctgagga	ggcaggagct	agagactgct	gtgagctcat	aggggtggga	agtttattcct	180
tcaagtcccg	cccaactcata	actgcttctc	accttccctt	gaccaggctt	acaagtgggt	240
tcttgcctgc	tttccctttg	gacccaacaa	gcccctgtaa	tgagtgtgca	tgactctgac	300
agctgtggac	tcagggctct	tggctacagc	tgccatgtaa	aatatctcat	ccagttctcg	360
caaattgtta	aaataaccac	atttcttaga	ttccagtacc	caaatcatgt	ctttacgaac	420
tgctcctcac	acccagaagt	ggcacaataa	ttcttgggaa	attattactt	tttttttct	480
ctctntnnnc	gnnngnnnng	gnnngnccag	gaattaccac	nttggaaagac	ctggccngaa	540
tttattat	aggggagccg	attnttttc	ctaacacaaa	gcgggtca		588

<210> 263

<211> 730

<212> DNA

<213> *Homo sapien*

<220>

<221> misc_feature

<222> (1) . . . (730)

<223> n = A, T, C or G

<400> 263

tttttttttt ttggcctga gcaactgaaa ttatgaaatt tccatatact caaaagagta 60
agactgcaaa aagattaaat gtaaaaagttg tcttgtatac agtaatgtt aagataccct 120
ttanatttat aaatggaaaa ttagggcatt tggatataca agttgaaaat tcaggagtga 180
ggttgggctg gctgggtata tactgaaaac tgcgtacatc cagatgacat ctaaaaccac 240
aaatctggtt ttatTTtagc agtgatatgt gtcactccca caaaagcctt cccattggc 300
ctcagcatac acaacaagtc acctccccac agccctctac acataaaacaa attccttagt 360
ttagttcagg aggaaatgcg ccctttcct tccgctctag gtgaccgcaa ggcccagttc 420
tcgtcaccaa gatgttaagg gaagtctgcc aaagaggcat ctgaaaggaa ataagggaa 480
tgggagtgac cacaaggaa agccaaggan aaactttgga gaccgttct agancctgg 540
catttcacaa caaaaactcng gaacaaacct tgcgtacatc atcatttaag ccctcggtt 600
ggannagact ttctgaactg ggccgtgaac ataancctca ttgaatgtct tcacagtctc 660
ccagctgaag gcacacccctt ggccagaagg ggaatcttcc aggtcctcaa nacagggctc 720
gccctttgnc 730

<210> 264

<211> 715

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (715)

<223> n = A, T, C or G

<400> 264

tttttttttt tttggccagt atgatagtct ctaccactat attgaagctc ttaggtcatt	60
tacacttaat gtggtatag atgctgttga gcttacttctt accaccttgc tatttctccc	120
gtctcttttt tgttcccttt ctcttctttt cctcccttat tttataattt aatttttttag	180
gattctattt tatatagatt tattcgttat aacactttgtt attctttgtt tttgtgggtc	240
ttctgtcatt tcaatgtgca tcttaaactc atcacaatctt atttcaaat aatatcatat	300
aaccttacat ataatgtttaa aatctaccac catatatttc catttctccc ttccatccta	360
tgtntgtcat atttttcctt ttatataatgtt tttaaagaca taatgtata tggaggttt	420
ttgcttaaaa tgtatcaat attccttcaa ngaaacgtaa aaattcaaaa taaatntctg	480
tttattctca aatnnnaccta atatttccta ccatntctna tacntttcaa gaatctgaag	540
gcattgggtt tttccggctt aagaacctcc tctaaagcac tctaaggcaga attaagtctt	600
ctgggagagg aattctccca agcttgggccc tttnanntgta ctccnntnang gttaaanttt	660
ggccgggaaa tagaaattcc aagttAACAG gntantttt nttnnttn tcncc	715

<210> 265

<211> 152

<212> DNA

<213> Homo sapien

<400> 265

tttttttttt tttcccaaca caaaggcacca ttatctttcc tcacaattttt caacatagtt	60
tgattcccat gaagagggtta tgatttctaa agaaaacatg gctactatac tatcaatcag	120
ggttaaatct ttttttttta agacggagtt ta	152

<210> 266

<211> 193

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1) ... (193)

<223> n = A, T, C or G

<400> 266

taaaactccgt ccccttctta atcaatatgg aggctaccca ctccacatata ctttcttttc	60
aagggactgt ttccgttaact gttgtgggtt ttcacgacca ggcttctaaa cttttaaaa	120
ctcccccaattt ctgggtgccaa cttggacaac atgctttttt tttttttttt ttttttttn	180
gagacggagt tta	193

<210> 267

<211> 460

<212> DNA

<213> Homo sapien

<400> 267

tgttgcgatc ccttaaggcat ggggtgttattt aaaaaatgg tggagaagaa aatacctgga	60
atttacgtct tatctttaga gattgggaag accctgtatgg aggacgtgga gaacagcttc	120

ttcttgaatg tcaattccca agtaacaaca gtgtgtcagg cacttgctaa ggatcctaaa	180
ttgcagcaag gctacaatgc tatgggattc tcccaggag gccaatttct gagggcagtg	240
gctcagagat gcccctcacc tcccatgatc aatctgatct cggttgggg acaacatcaa	300
ggtgttttg gactccctcg atgcccagga gagagctctc acatctgtga cttcatccga	360
aaaacactga atgctgggc gtactccaaa gttgttcagg aacgcctcgt gcaagccgaa	420
tactggcatg acccataaaa ggaggatgtg gatcgcaaca	460
<210> 268	
<211> 533	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1) ... (533)	
<223> n = A, T, C or G	
<400> 268	
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accttcgccc gtggggaccc cgagtacgtc tacggcgtcg tcacttagag taccoctctgg	120
acgcccgggc gcgttcgatt taccggaaagc gcgagctgca gtgggcttgc gccccccggcc	180
aaattctttg gggggtttaa gcccgcggg aatttgaggt atctctatca gtatgttagcc	240
aagttgaaac agtcggcatt cccgaaatcg ctttcttga atccgcaccc cctccagcat	300
tgcctcattc atcaacctga aggacacgcat aagtgacggt ttgttcttca gcagctccac	360
tccataacta gcgcgctcga cctcgtctc gtacgcgcca ggtccgtgcg tgcaattcc	420
caactccggt gagttgcgca tttcaagtn cgaaactgtt cgcctccacn atttggcatg	480
ttcacgcatg acacggaata aactcggttca gtaccggaa tggatcgca aca	533
<210> 269	
<211> 50	
<212> DNA	
<213> Homo sapien	
<400> 269	
ttttttttttt ttgcctgaa ttagctacag atcctcctca caagcggtca	50
<210> 270	
<211> 519	
<212> DNA	
<213> Homo sapien	
<400> 270	
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gctgagtcac gtgaacggtc agtgcaagca gccgcgtgcc agagcagagg tgcagcatgc	120
tgcacaccag ctcaggcgtg acctcctcca gcagatggc caggatggag ctgcgtacg	180
tgtccaccac ctccctggcac tttccgaca gggacttcgg cagcttcgag cacattttgt	240
caaaagcgtc gagtatttct ttctcagttc tggttggtc aatcagttt gtcacccct	300
tcaccaggaa ttcacacacc tcacagtaaa catcagactt tgctgggacc tcgtgcttct	360
taatgggctc caccagtcc agggcaggaa tgacattctt ggaggccact ttggcgggaa	420
ccagagtctg catgggcatac tcttcacact catcacagaa cccaaaccagc gcacagatct	480
ccttgggttg catgtgcatac atcatctggg atcgcacaca	519

<210> 271
 <211> 457
 <212> DNA
 <213> Homo sapien

<400> 271

ttttttttttt	ttcggggcggc	gaccggacgt	gcactcctcc	agtagcggct	gcacgtcg	60
ccaatggccc	gctatgagga	gttgagcgtg	tccggcttcg	aggagttcca	ccggggccgtg	120
gaacagcaca	atggcaagac	cattttcgcc	tacttacgg	gttctaagga	cgggggggggg	180
aaaagctgg	gccccgactg	cgtgcaggt	gaaccagtgc	tacgagaggg	gctgaagcac	240
attagtgaag	gatgtgtgtt	catctactgc	caagtaggag	aagagcctta	ttggaaagat	300
ccaaataatg	acttcagaaa	aaacttgaaa	gtaacagcag	tgcctacact	acttaagtat	360
ggaacaccc	aaaaactgg	agaatctgag	tgtcttcagg	ccaacctgg	ggaaatgttg	420
ttctctgaag	attaagattt	taggatggca	atcaaga			457

<210> 272
 <211> 102
 <212> DNA
 <213> Homo sapien

<400> 272

ttttttttttt	ttgggcaaca	acctgaatac	ctttcaagg	ctctggcttg	ggctcaagcc	60
cgcagggaa	atgcaactgg	ccaggtcaca	gggcaatcaa	ga		102

<210> 273
 <211> 455
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(455)
 <223> n = A,T,C or G

<400> 273

ttttttttttt	ttggcaatca	acaggttaa	gtcttcggcc	gaagttaatc	tcgtgttttt	60
ggcaatcaac	aggtttaagt	ttcggccga	agttaatctc	gtgtttttgg	caatcaacag	120
gtttaagtct	tcggccgaag	ttaatctcg	gtttttggca	atcaacaggt	ttaagtcttc	180
ggccgaagtt	aatctcggt	ttttggcaat	caacaggttt	aagtcttcgg	ccgaagttaa	240
tctcggttt	ttggcaatca	acaggttaa	gtcttcggcc	gaagttaatc	tcgtgttttt	300
ggcaatcaag	aggtttaagt	ttcggccga	agttaatctc	gtgtttttgg	caatcaacag	360
gtttaagtct	tcggccgaan	ttaatctcg	gtttttggca	atcaacaggt	ttaantcttc	420
ggccgaagtt	aatctcggt	ttttggcaat	caana			455

<210> 274
 <211> 461
 <212> DNA
 <213> Homo sapien

<400> 274

tttttttttt ttggccaata cccttgatga acatcaatgt gaaaatcctc ggtaaaatac	60
tggcaaacc aatccagcag cacatcaaaa agcttatcca ccatgatcaa gtgggcttca	120
tccctggat gcaaggctgg ttcaacataa gaaaatcaat aaatgtaatc catcacataa	180
acagaaccaa agacaaaaac cacatgatta tctcaataga tgcagaaaag gccttggaca	240
aattcaacag cccttcatgc taaacactct taataaaacta gatattgtatg gaatgtatct	300
caaataata agagctattt atgacaaaacc cacagccaat atcatactga atgggcaaag	360
actggaaagca ttccccttga aaactggcac aagacaagga tgccctctc caccgctcct	420
attcaacata gtatttggaaag ttctggccag ggcaatcaag a	461
<210> 275	
<211> 729	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(729)	
<223> n = A,T,C or G	
<400> 275	
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catgaaaaca taggaagggt gctgttacag caaacatttc agatagacga atcggccaag	120
ctccccaaac cccaccttca cagccttcc cacacgtctc ccanagattt gttgccttca	180
cttgcaaatt canggatgtt ggaagtngac atttnnagtn gcnggaaccc catcagtgaa	240
ncantaagca gaantacgt gactttgana nacanctgtat gaagaacacn ctacnganaa	300
ccctttctnt cgtgttanga tctcnngtcc ntcaactatg cggccccctg cnggtccacc	360
atttgggaga actccccccn cgttgatcc ccccttgagt ntcccattct ngtcccccan	420
accngncttg nngncantn cnncctcnca ccntgtttcc ctgnngtnaa aatnnngttt	480
nccgcncccc naattcccac ccnaatcaca gcbaanccng aaggcctcn naagtgtta	540
angcccnngng gtttcctcnnt ntanttgcag cttaccctcc cnctnnnnnt tncgngtgg	600
tcgcgcctg gncncgcctn gttcctctt nnggnnacaa cctngntcnn nggcncntcn	660
nnnctnttcc tnnnactagc tngcctntcc ncncgngn ncaangcaca ttncncnac	720
tntgtnncc	729
<210> 276	
<211> 339	
<212> DNA	
<213> Homo sapien	
<400> 276	
tgacctgaca tgttagtagat acttaataaaa tatttggat atgaatggat gaagtggagt	60
tacagagaaa aatagaaaaag tacaaattgt tgtcagtgtt ttgaaggaaa attatgtatct	120
ttcccaaaagt tctgacttca ttctaaagaca gggtagtat ctccatacat aatttactt	180
gctttgaaa atcaaatggag ataatctatt tagattgata atttatttag actggctata	240
aactattaag tgcttagcaaa tatacatttt aatctcat tccaccttcc gtgatatacg	300
tatgttaggtt ttgactttaa tggatgtcag gtcaatccc	339
<210> 277	
<211> 664	
<212> DNA	
<213> Homo sapien	

<220>
 <221> misc_feature
 <222> (1)...(664)
 <223> n = A,T,C or G

<400> 277

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aagcatccaa	aggaaacaaa	tgatggtaag	accgtgccaa	gtggggagca	gacaccaaag	120
taagaccaca	gatttacat	tcaacaggtt	gctcacagta	cttgcccgaa	cactgtggc	180
agaaatagcc	tcctaatgtt	agccctggct	cagtattgcc	atccaaatgc	gccatgctga	240
aagagggtt	tgcattctgg	ttagatnaag	aagcaatggt	gtgctgagga	aatccatac	300
gaataagtga	gcattcagaa	ctttagctag	caggaggagg	actaagatga	tgtgtgagca	360
actctttgtt	atggcttca	tctaaaataa	catggtacgt	gccaccagt	tcacgagcaa	420
gtacagtgtc	aacgcgaact	tctgcagaca	atccaaataac	agataactcta	attttagctg	480
cctttaggg	ttttagtttt	tctaaaat	tagatggatc	gcaagttgt	aggntgctaa	540
aagatgatta	gtacttctcg	acttgtatgt	ccaggcatgt	tgttttaan	tctgccttag	600
ccctgctta	ggggaaatttt	taaagaagat	ggctctccat	gttcanggtc	aatcacnaat	660
tgcc						664

<210> 278

<211> 452
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(452)
 <223> n = A,T,C or G

<400> 278

tgacctgaca	ttttagggaa	gcacacaccc	ctgaaattcc	tttagtttag	aagggcattt	60
gacacagagt	gggcctctga	taattcatga	aatgcattct	gaagtcattcc	agaatggagg	120
ctgcaatctg	ctgtgtttt	ggggtttgct	cactgtgtc	ctggatatac	cacaaaagct	180
gcaatccctc	tttttcaact	aacatttgc	agtatttgct	gggatttta	ctgcagacat	240
gatacatagc	ccatagtgtc	cagagctgaa	cctctgggtt	agagaagttt	ccaaggagcg	300
ggaaaaatgt	ttttagtttt	ctataggc	ccaatgtgt	catcttacaa	cttgaacttg	360
cccaattctg	tatgggttgc	tgcagatctt	ggagaagagt	acgcctctgg	aagtacacggg	420
atatccaaan	ctgtctgtca	gatgtcagg	ca			452

<210> 279

<211> 274
 <212> DNA
 <213> Homo sapien

<400> 279

tttttttttt	ttcgccaagg	caaatttact	tctgaaaag	ggtgctgtt	gcactttgg	60
ccactgcgag	agcacaccaa	acaaaagttag	gaaggggtt	ttatccctaa	cgcggttatt	120
ccctgggttct	gtgtctgtc	cccattggct	ggagtcagac	tgcacaaatct	acactgaccc	180
aactggctac	tgtttaaaat	tgaatatgaa	taatttaggtt	ggaaggggaa	ggctgtttgt	240
tacggtacaa	gacgtgtttt	ggcatgtcag	gtca			274

<210> 280
 <211> 272
 <212> DNA
 <213> Homo sapien

<400> 280
 tacctgacat ggagaaaataa cttgttagtat tttgcgtgca atggaataact atatgagggt 60
 gaaaaatgaat gaactagcaa tgcgtgtatc aacatgaata aatccccaaa acataataat 120
 gttgaatgga aaaggtgagt ttcagaagga tatatatgcc ctctaaatcc atttatgtaa 180
 acctttaaaaa aactacatta tttatggtca taagtccatc cagaaaaatat taaaaaacct 240
 acatgggatt gataactact gatgtcaggt ca 272

<210> 281
 <211> 431
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(431)
 <223> n = A,T,C or G

<400> 281
 tttttttttt ttggccaata gcatgattta aacattggaa aaagtcaa at gagaatgcg 60
 aatttttatg ttctcttgc aaatcaaaag agtaggcaac attggttcct cattcttgaa 120
 tagcattaaat cagaaaaat tgcatacgct ctagcctcct tagagtaggt gtgtcttc 180
 aaatatatca tagtcccaca gtttattttca tgtatatttt ctgcctgaat cacatagaca 240
 tttgaatttg caacgcctga tgtaaatata taaattctta ccaatcagaa acatagcaag 300
 aaattcaggg acttggtcat yatcagggt tgacagcana tccctgtara aacactgata 360
 cacactcaca cacgtatgca acgtggagat gtcgcyyttww kkktwywcwm rmrycrwcgn 420
 aatcacttan n 431

<210> 282
 <211> 98
 <212> DNA
 <213> Homo sapien

<400> 282
 attcgattcg atgcttgagc ccaggagttc aagactgcag tgagccactg cacttcaggc 60
 tggacaacag agcgagtccc tgtgccaaaa aaaaaaaaaa 98

<210> 283
 <211> 764
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(764)
 <223> n = A,T,C or G

<400> 283	
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tataaaactgc tgtatctagg ggcaggacca agggggcagg ggcaacagcc ccagcgtgca	120
gggccascat tgcacagtgg astgcaaagg ttgcaggcta tgggcggcta ctavtaaccc	180
cgttttcct gtattatctg taacataata tggtagactg tcacagagcc gaatwccart	240
hacasgatga atccaawggt caygaggatg cccasaatca gggcccasat sttcaggcac	300
ttggcggtgg gggcatasgc ctgkgccccg gtcacgtcsc caaccwtcty cctgtcccta	360
cmcttgawtc cncncctnn nntncntna tntgcccgc cncctctng ngtcaaccng	420
natctgact anctccctcn cccctntgg antctcntcc ttcaantaan nttatccttn	480
acnccccct cnccttccc ctnccnccn tnatccngn nccnctatca ntcntnccct	540
cnctntnctn cnnatcggtc cncctnntaa ctacncttn nacnannct cactnatncc	600
ngnnanttct ttccctccct cccnacgcnn tgctgcgcg cgtctngct nnctnccgna	660
cccnacttt atttacctt ncaccctagc nctctacttn acccancnc tcctacctcc	720
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<210> 284	
<211> 157	
<212> DNA	
<213> Homo sapien	
<400> 284	
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atttctcccc ttccaggaac gtcttgcattg gatgatcaa gatcagctcc tggtaacat	120
aaataagcta gtttaagata cgttccctta cacttga	157
<210> 285	
<211> 150	
<212> DNA	
<213> Homo sapien	
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<213> Homo sapien	
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taggtactga agattcaagt gaccgagatg ctagcccttg ggttcaagtg atccctctcc	180	
cagagtgcac tggactgaa	199	
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aa	182	
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<210> 291
 <211> 1851
 <212> DNA
 <213> Homo sapien

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tcacttcctt taagcctttg tgactcttcc tctgtatgtca gctttaagtc ttgttctgga	180
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caaattacat gatgtgact agaaacagca tactctctgg ccgtctttcc agatcttgag	300
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ttggatcagt gccatgttcc agcaacatca acgcacattt atcttcctgg cattgtacgg	660
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cttttccca ttttagtattt tggtggctgtt gggcttgc taggtgggtt ttattacttt	1800
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<210> 292
 <211> 1851
 <212> DNA
 <213> Homo sapien

<400> 292

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ttgctgttt	cagaagagat	ttttaacatc	tgttttctt	tgttagtcaga	aagtaactgg	240
caaattacat	gatgtgact	agaaacagca	tactctctgg	ccgtctttcc	agatcttgag	300
aagatacatc	aacatttgc	tcaagttagag	ggctgactat	acttgctgtat	ccacaacata	360
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<210> 293

<211> 668

<212> DNA

<213> Homo sapien

<400> 293

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catatcttag	gaattcaaaa	taacattcca	cagcttcac	caactagttt	tattaaagg	360
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gcagtcctat gagagtgaga agactttta ggaaattgtt gtgcactagc tacagccata	600
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aaaaaaaaaa	668

<210> 294
 <211> 1512
 <212> DNA
 <213> Homo sapien

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<210> 295
 <211> 1853
 <212> DNA
 <213> Homo sapien

<400> 295	
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<210> 296
 <211> 2184
 <212> DNA
 <213> Homo sapien

<400> 296

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<210> 297
 <211> 1855
 <212> DNA
 <213> Homo sapien

 <220>
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 <223> n = A,T,C or G

<400> 297						
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caacgcacg	ttgcacgcgc	ggcagcggt	tggctggctt	gtaacggctt	gcacgcgcac	120
ggcccccgg	cataaccgtc	agactggct	gtaacggctt	gcaggcgcac	gccgcacgc	180
cgttaacgggt	tggctgcct	gtaacggctt	gcaacgtgc	gctgcacgc	cgttaacggc	240
ttggctggca	tgttagccgt	tggctggct	ttgcattttt	tgctkggctk	ggcgttgkty	300
tcttggattt	acgcttcctc	tttggatkga	cgtttccctc	tttggatkgac	gtttcytyty	360
tcgcgttcc	ttgctggact	tgacctttt	tctgtgggt	tttgcattcc	tttgggggtgg	420
gtctgggtgtt	tttccgggg	gggkkgcccc	tttccgggtt	gggcgtgggk	cgccccccagg	480
gggcgtggg	tttccccggg	ttgggtgtgg	ttttccctgg	ttgggtgtgg	ctgtgtgtgg	540
atccccctgc	ttgggttggc	agggatttgc	tttttcttc	aaacagatttgc	gaaacccgg	600
gtaacntgt	agttggtaa	actgggttgt	agacgcgtc	tgctgtact	actgtttctc	660
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agaaggccatt	tggtctcagg	agcaagatgg	gcaagtgggt	cgccactgt	tccctgtctg	780
cagggggagc	ggcaagagca	acgtgggcac	ttctggagac	cacaacgact	cctctgtgaa	840
gacgcttgg	agcaagaggt	gcaagtgggt	ctgcccactg	tttcccctgc	tgcaagggag	900
cgcaagagc	aacgtggkcg	tttggggaga	ctacatgac	agcgccttca	tggakcccag	960
gtaccacgtc	crtggagaag	atctggacaa	gctccacaga	gctgcctggt	ggggtaaagt	1020
ccccagaaag	gatctcatcg	tcatgtcg	ggacactgay	gtgaacaaga	rggacaagca	1080
aaagaggact	gctctacatc	tggcctctgc	caatggaaat	tcagaagtag	taaaactcg	1140
gctggacaga	cgatgtcaac	ttaatgtcct	tgacaacaaa	aagaggacag	ctctgacaaa	1200
ggccgtacaa	tgccaggaag	atgaatgtgc	gttaatgttg	ctggaacatg	gcactgtatcc	1260

aaatattcca gatgagtatg gaaataccac tctacactat gctgtctaca atgaagataa	1320
attaatggcc aaagcactgc tcttatacgg tgctgatatac gaatcaaaaa acaaggtata	1380
gatctactaa ttttatcttc aaaatactga aatgcattca ttttaacatt gacgtgtgt	1440
agggccagtc ttccgtatTTT ggaagctcaa gcataacttg aatgaaaata ttttggaaatg	1500
acctaattat ctaagacttt attttaaata ttgttatttt caaagaagca ttagaggta	1560
cagttttttt tttttaaatg cacttctggT aaatactttt gttgaaaaca ctgaatttgt	1620
aaaaggtaat acttactatt ttcaattttt tccctccatg gatTTTTTC ccctaattgaa	1680
tgttaagatgg caaaaatttgc cctgaaatag gtttacatg aaaaactccaa gaaaagttaa	1740
acatgtttca gtgaatagag atcctgctcc tttggcaagt tcctaaaaaa cagtaataga	1800
tacgaggtga tgccctgtc agtggcaagg tttaagatat ttctgatctc gtgcc	1855

<210> 298
 <211> 1059
 <212> DNA
 <213> Homo sapien

<400> 298

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gogcttgrgg agactmcgt gacagygctt tcattggagcc caggtaccac gtccgtggag	180
aagatctgga caagctccac agagctgccc tgggtgggta aagtccccag aaaggatctc	240
atcgtcatgc tcaggacac tgggtgtgaac aagarggaca agcaaaagag gactgctcta	300
catctggccct ctgccaatgg gaattcagaa gtagtaaaac tcstgctgga cagacgatgt	360
caacttaatg tccttgacaa caaaaagagg acagctctga yaaaggccgt acaatgccag	420
gaagatgaat gtgcgttaat gttgctggaa catggcactg atccaaatat tccagatgag	480
tatggaaata ccactctrca ctaygctrca tayaatgaag ataaattaaat ggccaaagca	540
ctgctcttat aygggtgtga tatcaatca aaaaacaagg tatagatcta ctaattttat	600
cttcaaaata ctgaaatgca ttcattttaa cattgacgtg tgtaaggccc agtcttcgt	660
atttggaaagc tcaagcataa cttgaatgaa aatattttga aatgacctaa ttatctaaga	720
ctttattttta aatattgtta ttttcaaaga agcattagag ggtacagtt tttttttta	780
aatgcacttc tggtaataac ttttggtaa aacactgaat ttgtaaaagg taataacttac	840
tatTTTTCAA tttttccctc cttagatttt tttccctaa tgaatgtaa atggccaaat	900
ttggccctgaa ataggtttta catgaaaact ccaagaaaag ttaaacatgt ttcaatgt	960
agagatcctg ctcccttggc aagttctaa aaaacagtaa tagatacgtg gtgatgcgccc	1020
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<210> 299
 <211> 329
 <212> PRT
 <213> Homo sapien

<400> 299

Met Asp Ile Val Val Ser Gly Ser His Pro Leu Trp Val Asp Ser Phe	
1 5 10 15	
Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu	
20 25 30	
Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser	
35 40 45	
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg	
50 55 60	
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val	

65	70	75	80
Val Leu Pro Leu Leu Pro	Leu Leu Gln Gly Ser	Gly Lys Ser Asn Val	
	85	90	95
Val Ala Trp Gly Asp Tyr Asp Asp	Ser Ala Phe Met Asp	Pro Arg Tyr	
	100	105	110
His Val His Gly Glu Asp Leu Asp	Lys Leu His Arg Ala	Ala Trp Trp	
	115	120	125
Gly Lys Val Pro Arg Lys Asp	Leu Ile Val Met Leu	Arg Asp Thr Asp	
	130	135	140
Val Asn Lys Arg Asp Lys Gln	Lys Arg Thr Ala	Leu His Leu Ala Ser	
	145	150	160
Ala Asn Gly Asn Ser Glu Val Val	Lys Leu Val Leu	Asp Arg Arg Cys	
	165	170	175
Gln Leu Asn Val Leu Asp Asn Lys	Lys Arg Thr Ala	Leu Thr Lys Ala	
	180	185	190
Val Gln Cys Gln Glu Asp Glu Cys	Ala Leu Met Leu	Leu Glu His Gly	
	195	200	205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr	Gly Asn Thr Thr	Leu His Tyr	
	210	215	220
Ala Val Tyr Asn Glu Asp Lys Leu	Met Ala Lys Ala	Leu Leu Leu Tyr	
	225	230	240
Gly Ala Asp Ile Glu Ser Lys Asn Lys	His Gly Leu Thr	Pro Leu Leu	
	245	250	255
Leu Gly Ile His Glu Gln Lys Gln	Gln Val Val Lys	Phe Leu Ile Lys	
	260	265	270
Lys Lys Ala Asn Leu Asn Ala Leu	Asp Arg Tyr Gly	Arg Thr Ala Leu	
	275	280	285
Ile Leu Ala Val Cys Cys Gly Ser	Ala Ser Ile Val	Ser Pro Leu Leu	
	290	295	300
Glu Gln Asn Val Asp Val Ser Ser	Gln Asp Leu	Glu Arg Arg Pro Glu	
	305	310	320
Ser Met Leu Phe Leu Val Ile Ile	Met		
	325		

<210> 300
<211> 148
<212> PRT
<213> *Homo sapien*

<220>
<221> VARIANT
<222> (1)...(148)
<223> Xaa = Any Amino Acid

<400> 300

Met	Thr	Xaa	Pro	Ser	Trp	Ser	Pro	Gly	Thr	Thr	Ser	Val	Glu	Lys	Ile
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Trp	Thr	Ser	Ser	Thr	Glu	Leu	Pro	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys
								20		25				30	
Asp	Leu	Ile	Val	Met	Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Xaa	Asp	Lys
							35		40				45		

Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
 50 55 60
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
 65 70 75 80
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
 85 90 95
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
 100 105 110
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
 115 120 125
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser
 130 135 140
 Lys Asn Lys Val
 145

<210> 301
 <211> 1155
 <212> DNA
 <213> Homo sapien

<400> 301

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agcaacgtgg	gcacttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
atggggcaagt	ggtcgcgcca	ctgctcccc	tgctgcaggg	ggagtggcaa	gagcaacgtg	240
ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	atggggcaag	300
tgtgtctg	actgcttccc	ctgctgcagg	ggagcggca	agagcaaggt	ggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccaggtacc	acgtccgtgg	agaagatctg	420
gacaagctcc	acagagctgc	ctgggggggt	aaagtcccc	gaaaggatct	catgtcatg	480
ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaga	ggactgctct	acatctggcc	540
tctgccaatg	ggaattcaga	agtagtaaaa	ctcctgctgg	acagacgtg	tcaacttaat	600
gtccttgaca	acaaaaagag	gacagctctg	ataaaggccg	tacaatgcca	ggaagatgaa	660
tgtgcgtta	tgttgcggaa	acatggact	gatccaaata	ttccagatga	gtatggaaat	720
accactctgc	actacgttat	ctataatgaa	gataaaattaa	tggccaaagc	actgcttta	780
tatggtgctg	atatcgaatc	aaaaaacaag	catggcctca	caccactgtt	atgggtgtta	840
catgagcaaa	aacagaagt	cgtgaaattt	ttaatcaaga	aaaaagcgaa	tttaatgca	900
ctggatagat	atggaaggac	tgctctcata	cttgcgttat	gttgcggatc	agcaagtata	960
gtcagccttc	tacttgagca	aaatattgtat	gtatcttc	aagatctatac	tggacagacg	1020
gccagagagt	atgcttttc	tagtcatcat	catgtatattt	gccagttact	ttctgactac	1080
aaagaaaaac	agatgctaaa	aatctttct	gaaaacagca	atccagaaaa	tgtctcaaga	1140
accagaaata	aataa					1155

<210> 302

<211> 2000

<212> DNA

<213> Homo sapien

<400> 302

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agcaacgtgg	gcacttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180

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ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag
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ggagactacg atgacagtgc cttcatggag cccaggtacc acgtccgtgg agaagatctg
gacaagctcc acagagctgc ctgggtgggt aaagtccccaa gaaaggatct catcgcatg
ctcagggaca ctgacgtgaa caagaaggac aagcaaaaaga ggactgctct acatctggcc
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gtcagccttc tacttgagca aaatattgat gtatcttctc aagatcttac tggacagacg
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aaaaaaaaaaaa aaaaaaaaaaaaa

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<210> 303
<211> 2040
<212> DNA
<213> Homo sapien
```

<400> 303

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agcaacgtgg	gcacttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
atgggcaagt	ggttccggca	ctgtttcccc	tgtgcagggg	ggagtggcaa	gagcaacgtg	240
ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
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ggagactacg	atgacagtgc	cttcatggag	cccaggta	acgtccgtgg	agaagatctg	420
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ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaga	ggactgctct	acatctggcc	540
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accactctqc	actacgctat	ctataatgaa	gataaaattaa	tggccaaagc	actgcttta	780

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caagaaccag aaataaataa	ggatggtgat	agagagctag	aaaattttat	ggctatcgaa	1620
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gaaaaagaca tcttgcata	aaatagtacg	ttgcgggaag	aaattgcoat	gctaagactg	1980
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<210> 304

<211> 384

<212> PRT

<213> Homo sapien

<400> 304

Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser	Ser	Val	Lys	Lys	
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Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe	
							20			25				30		
Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp	
							35			40				45		
His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	
						50			55				60			
Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val	
						65			70				75		80	
Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn	
						85							90		95	
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	
							100			105				110		
Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe	
							115			120				125		
Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His	
							130			135				140		
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met	
							145			150				155		160
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala	
							165			170				175		
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu	

180	185	190	
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys	Lys Arg Thr		
195	200	205	
Ala Leu Ile Lys Ala Val Gln Cys Glu Asp Glu Cys Ala	Leu Met		
210	215	220	
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu	Tyr Gly Asn		
225	230	235	240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys	Leu Met Ala Lys		
245	250	255	
Ala Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys	His Gly		
260	265	270	
Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys	Gln Val Val		
275	280	285	
Lys Phe Leu Ile Lys Lys Ala Asn Leu Asn Ala Leu Asp	Arg Tyr		
290	295	300	
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly	Ser Ala Ser Ile		
305	310	315	320
Val Ser Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln	Asp Leu		
325	330	335	
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His	His His Val		
340	345	350	
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met	Leu Lys Ile		
355	360	365	
Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg	Thr Arg Asn Lys		
370	375	380	

<210> 305

<211> 656

<212> PRT

<213> Homo sapien

<400> 305

Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val	Lys Lys		
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Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys	Arg Cys Phe		
20	25	30	
Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly	Thr Ser Gly Asp		
35	40	45	
His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met	Gly Lys Trp		
50	55	60	
Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly	Lys Ser Asn Val		
65	70	75	80
Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys	Thr Leu Arg Asn		
85	90	95	
Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys	Cys Arg Gly Ser		
100	105	110	
Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp	Asp Ser Ala Phe		
115	120	125	
Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp	Leu Asp Lys Leu His		
130	135	140	
Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp	Leu Ile Val Met		

145	150	155	160
Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala			
165	170	175	
Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu			
180	185	190	
Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr			
195	200	205	
Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met			
210	215	220	
Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn			
225	230	235	240
Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys			
245	250	255	
Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly			
260	265	270	
Leu Thr Pro Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val			
275	280	285	
Lys Phe Leu Ile Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr			
290	295	300	
Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile			
305	310	315	320
Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu			
325	330	335	
Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val			
340	345	350	
Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile			
355	360	365	
Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu			
370	375	380	
Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys			
385	390	395	400
Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu			
405	410	415	
Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn			
420	425	430	
Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro			
435	440	445	
Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu			
450	455	460	
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu			
465	470	475	480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp			
485	490	495	
Leu Lys Leu Thr Ser Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu			
500	505	510	
Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys			
515	520	525	
Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly			
530	535	540	
Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser			
545	550	555	560

Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr
 565 570 575
 His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln
 580 585 590
 Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln
 595 600 605
 Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys
 610 615 620
 Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile
 625 630 635 640
 Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
 645 650 655

<210> 306
 <211> 671
 <212> PRT
 <213> Homo sapien

<400> 306
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255

Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
 450 455 460
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
 465 470 475 480
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
 485 490 495
 Leu Lys Leu Thr Ser Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
 500 505 510
 Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp
 515 520 525
 Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys
 530 535 540
 His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala
 545 550 555 560
 Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg
 565 570 575
 Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His
 580 585 590
 Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn
 595 600 605
 Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile
 610 615 620
 Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys
 625 630 635 640
 Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala
 645 650 655
 Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu

660

665

670

<210> 307
 <211> 800
 <212> DNA
 <213> Homo sapien

<400> 307

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 agaatgctta ggactctaac aggttttga gaatgtttg gtaaggccca ctcaatccaa 180
 ttttcttgg tcctccttgc ggtctaggag gacaggcaag ggtcagatt ttcaagaatg 240
 catcagtaag ggccactaaa tccgacccctc ctcgttccctc cttgtggctt gggagggaaa 300
 ctatgtttc tggctgttgc tcaatgttca caactattcc gatcagcagg gtccaggggac 360
 cactgcagg tcttgggcag gggggaaaac aaaacaaacc aaaaccatgg gcrgtttgt 420
 ctttcagatg ggaaacactc aggcatcaac aggctcacct ttgaaatgca tcctaagcca 480
 atgggacaaa tttgacccac aaaccctgga aaaagaggtt gtcattttt tttgcactat 540
 ggcttggccc caacattctc tctctgtatgg ggaaaaatgg ccacctgagg gaagtacaga 600
 ttacaataact atcctgcagc ttgacccctt ctgttaagagg gaaggcaaat ggagtgaaat 660
 accttatgttc caagcttct tttcattgaa ggagaataca ctatgcaaag cttgaaattt 720
 acatcccaca ggaggaccc tcagcttacc cccatatcct agcctcccta tagctcccct 780
 tcctatttagt gataaggcctc 800

<210> 308

<211> 102
 <212> PRT
 <213> Homo sapien

<220>

<221> VARIANT
 <222> (1) ... (102)
 <223> Xaa = Any Amino Acid

<400> 308

Met	Gly	Xaa	Phe	Val	Phe	Gln	Met	Gly	Asn	Thr	Gln	Ala	Ser	Thr	Gly
1							5			10				15	
Ser	Pro	Leu	Lys	Cys	Ile	Leu	Ser	Gln	Trp	Asp	Lys	Phe	Asp	Pro	Gln
							20			25				30	
Thr	Leu	Glu	Lys	Glu	Val	Ala	His	Phe	Phe	Cys	Thr	Met	Ala	Trp	Pro
							35			40			45		
Gln	His	Ser	Leu	Ser	Asp	Gly	Glu	Lys	Trp	Pro	Pro	Glu	Gly	Ser	Thr
							50			55			60		
Asp	Tyr	Asn	Thr	Ile	Leu	Gln	Leu	Asp	Leu	Phe	Cys	Lys	Arg	Glu	Gly
65								70			75			80	
Lys	Trp	Ser	Glu	Ile	Pro	Tyr	Val	Gln	Ala	Phe	Phe	Ser	Leu	Lys	Glu
							85			90			95		
Asn	Thr	Leu	Cys	Lys	Ala										
					100										

<210> 309

<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 309

Leu Met Ala Glu Glu Tyr Thr Ile Val
1 5

<210> 310
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 310

Lys Leu Met Ala Lys Ala Leu Leu Leu
1 5

<210> 311
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 311

Gly Leu Thr Pro Leu Leu Leu Gly Ile
1 5

<210> 312
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 312

Lys Leu Val Leu Asp Arg Arg Cys Gln Leu
1 5 10

<210> 313
<211> 1852
<212> DNA
<213> Homo sapiens

<400> 313

ggcacgagaa ttaaaaaccct cagcaaaaca ggcatagaag ggacatacct taaagtaata 60
 aaaaccacct atgacaagcc cacagccaac ataatactaa atggggaaaa gttagaagca 120
 tttcctctga gaactgcaac aataaataca aggatgctgg attttgtcaa atgcctttc 180
 ttgtctgtt gagatgctta tgtgactttg ctttaattc tgtttatgtg attatcacat 240
 ttattgactt gcctgttta gaccggaaga gctgggggtgt ttctcaggag ccaccgtgtg 300
 ctgcggcagc ttccggataa ctggaggctg catcaactggg gaagaaaacac aytccctgtcc 360
 gtggcgctga tggctgagga cagagctca gtgtggcttc tctgcgactg gcttcttcgg 420
 ggagttcttc cttcatagtt catccatata gctccagagg aaaattata tattttgtta 480
 tggatgaaga gtattacgtt gtgcagatat actgcagtgt cttcatctt tgatgtgtga 540
 ttgggttaggt tccaccatgt tgccgcagat gacatgatt cagttacgtt gtctggctga 600
 aaagtgtttg tttgtgaatg gatattgtgg tttctggatc tcatacctctg tgggtggaca 660
 gcttctcca ctttgcgttga agtgacactgc tttccagaag tttgtatggct gaggagtata 720
 ccatcgtgca tgcattttc atttctgca tttcttcctc cttggatggc caggggggagc 780
 ggcagagca acgtggcac ttctggagac cacaacgact cttctgtgaa gacgottggg 840
 agcaagaggt gcaagtggtg ctggccactgc ttcccctgtc gcaggggggag cggcaagagc 900
 aacgtggcg cttgggaga ctacgatgac agcgccttca tggatcccg gtaccacgtc 960
 catggagaag atctggacaa gctccacaga gctgcctggt ggggtaaagt ccccaagaaag 1020
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 gctctacatc tggcctctgc caatggaaat tcagaagtag taaaactcgt gctggacaga 1140
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 tgccaggaag atgaatgtgc gttaatgttg ctggacatgc gcaactgatcc aaatattcca 1260
 gatgagttatg gaaataccac tctacactat gctgtctaca atgaagataa attaatggcc 1320
 aaagcactgc tcttatacgg tgctgatatc gaatcaaaaa acaagcatgg cctcacacca 1380
 ctgctacttg gtatacatga gcaaaaaacag caagtggta aatttttaat caagaaaaaaa 1440
 gcaatttaa atgcgttgg tagatatggc agaactgctc tcatacttgc tttatgttgc 1500
 ggtatcggaa gtatagtcag ccctctactt gagcaaaatg ttgtatgttgc ttctcaagat 1560
 ctggaaagac ggcagagag tatgctgtt ctgttcatca tcatacttgc tgccagttac 1620
 tttctgacta caaagaaaaa cagatgttaa aaatctttc tgaaaacagc aatccagaac 1680
 aagacttaaa gctgacatca gaggaagagt cacaaggct taaaggaagt gaaaacagcc 1740
 agccagagct agaagattta tggctattga agaagaatga agaacacggc agtactcatg 1800
 tgggattccc agaaaacctg actaacggtg ccgctgctgg caatggtgat ga 1852

<210> 314

<211> 879

<212> DNA

<213> Homo sapiens

<400> 314

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 aacgtggca cttctggaga ccacaacgac tcctctgtga agacgcttgg gagcaagagg 120
 tgcaagtggt gctgccactg cttcccttgc tgcaggggga gcccgaagag caacgtggc 180
 gcttggggag actacgtga cagcgccttc atggatccca ggtaccacgt ccatggagaa 240
 gatctggaca agctccacag agtgcctgg tgggtaaag tcccccagaaa ggatctcatc 300
 gtcatgctca gggacacggc tggtaacaag agggacaagc aaaagaggac tgctctacat 360
 ctggcctctg ccaatggaa ttcaagaatgtt gttaaaactcgt tgctggacag acgtatgtcaa 420
 cttaatgtcc ttgacaacaa aaagaggaca gctctgacaa aggccgtaca atgcaggaa 480
 gatgaatgtg cgttaatgtt gttggaaat ggcactgatc cttatattcc agatgagttat 540
 gggaaataccac ctctacacta tgctgtctac aatgaagata attaatggc caaagcactg 600
 ctcttatacg gtgctgtat cgttacaaa aacaaggatg gcctcacacc actgctactt 660
 ggtatacatg agcaaaaaaca gcaagtggtg aaatttttaa tcaagaaaaa agcgaattta 720

aatgcgctgg atagatatgg aagaactgct ctcatacttg ctgtatgttg tggatcagca 780
 agtatagtca gccctctact tgagcaaaat gttgatgtat cttctcaaga tctggaaaga 840
 cggccagaga gtatgctgtt tctagtcatc atcatgtaa 879

<210> 315
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 315
 Met His Leu Ser Phe Pro Ala Phe Leu Pro Pro Trp Met Asp Arg Gly
 5 10 15
 Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp His Asn Asp Ser Ser
 20 25 30
 Val Lys Thr Leu Gly Ser Lys Arg Cys Lys Trp Cys Cys His Cys Phe
 35 40 45
 Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val Val Ala Trp Gly Asp
 50 55 60
 Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu
 65 70 75 80
 Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg
 85 90 95
 Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Arg Asp
 100 105 110
 Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser
 115 120 125
 Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys Gln Leu Asn Val Leu
 130 135 140
 Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala Val Gln Cys Gln Glu
 145 150 155 160
 Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile
 165 170 175
 Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Val Tyr Asn Glu
 180 185 190
 Asp Lys Leu Met Ala Lys Ala Leu Leu Tyr Gly Ala Asp Ile Glu
 195 200 205
 Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Ile His Glu
 210 215 220

Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu
 225 230 235 240

Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys
 245 250 255

Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu Glu Gln Asn Val Asp
 260 265 270

Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu Ser Met Leu Phe Leu
 275 280 285

Val Ile Ile Met
 290

<210> 316
 <211> 584
 <212> DNA
 <213> Homo sapiens

<400> 316
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 tttttgtgg tccttggag atttcttgc ttatttctt ctgggtgggg gtgatttagag 120
 gaggcttatac actaatagga agggagcta tagggaggct aggatatggg ggttaagctga 180
 gaggtcctcc tgtggatgt aaatttcaag cttgcatacg tgtattctcc ttcaatgaaa 240
 agaaaagcttgc gacataaggt atttcactcc atttgccttc cctcttacag aaaaggtcaa 300
 gctgcaggat agtattgtaa tctgtacttc cctcagggtgg ccattttcc ccatcagaga 360
 gagaatgttg gggccaagcc atagtgcaga aaaaaaaaaatg agccacctct ttttccaggg 420
 tttgtgggtc aaatttgc tattggctt ggtatgcattt caaaggtagg cctgttgatg 480
 cctgagtgtt tcccatctga aagacaaaac tgcccatggt tttgggttgt tttgtttctc 540
 cccctgccc aagaactatca aactcctgag ccaacaacta aaaa 584

<210> 317
 <211> 829
 <212> DNA
 <213> Homo sapiens

<400> 317
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 acttcatttt tggtacataa catcttataa ggacagggtt aaaatccaa tactaacagg 120
 agaatgctta ggactctaac aggttttga gaatgtgtt gtaaggggcca ctcaatccaa 180
 ttttcttgg tcctccttgc ggtctaggag gacaggcaag ggtgcagatt ttcaagaatg 240
 catcagtaag ggccactaaa tccgaccttc ctcgttccctc cttgtggct gggaggaaaa 300
 ctatgtttc tggtgcgttgc tcaatgttcaacttcc gatcagcagg gtccaggag 360
 cactgcaggat tcttggcag ggggagaaaac aaaacaaacc aaaaccatgg gcagttttgt 420
 ctttcagatg ggaaacactc aggcatcaac aggctcacct ttgaaatgca tcctaagcc 480
 atgggacaaa tttgacccac aaaccctgga aaaagaggtg gtcattttt tttgcactat 540
 ggcttggccc caacatttctc tctctgttgg ggaaaaatgg ccacctgagg gaagtacaga 600
 ttacaatact atcctgcagc ttgacctttt ctgtaagagg gaaggcaaattt ggagtgaaat 660
 accttatgtc caagtttctt ttcattgaa ggagaataca ctatgcaaag cttgaaattt 720

acatcccaca ggaggacctc tcagcttacc cccatatacct agcctcccta tagctccct 780
tccttattgt gataaggcctc ctctaatcac ccccacccag aagaaaata 829